Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

http://www.pir.uniprot.org/database/archive.shtml

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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GenCore Copyright (c) 1993 protein - protein sew	version 5.1.6 - 2005 Compugen Ltd. • model	30 72.5 5.6 156 2 H71623 probable secreted 31 72.5 5.6 218 2 A99014 hypothetical prote 32 72.5 5.6 243 2 A99387 schedendent meth 33 71.5 5.6 195 1 140422 conserved hypothet 34 71.5 5.6 227 2 H64336 formate achydrogen 35 71.5 5.34 2 T21543 hypothetical prote
June 3, 2005, 06:3	3	70.5 5.5 189 chitchest 77.5 5.5 22.2 737839 hypothetical 77.5 5.5 22.6 2 C81749 conserved by 77.5 5.4 209 2 199593 lipoprotein 1
Title: US-10-662-431-2_COPY_3 Perfect BCOXe: 1287 Sequence: 1 TNBLKQMQDKYSKSGIACFL	39_281 TLNEHLIDMDHEASFFGAFLVG 243	69.5 5.4 199 2 69.5 5.4 201 2 69.5 69.5 6.4 202 2
table: BLOSUM62 Gapop 10.0 , Gapext 0	s.:	69 5.4 139 2 T28300
earched: 283416 segs, 96216763	residues	ALIGNMENTS
number of hits satisfying chose	chosen parameters: 125689	י ה הוספם
DB seq length: 0 DB seq length: 243		SANCES AND ACTOR DESCRIPTION - DIG
Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 sum	0% 100% 45 summaries	C;Species: Sus scrota domestica (domestic pig) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004 C;Accession: S17289 R;Kuhnert, P.; Wuethrich, C.; Peterhans, E.; Pauli, U.
Database : $PIR_79:*$ 1: $\overrightarrow{p}ixI:*$ 2: $pix2:*$ 3: $pix2:*$ 4: $pix4:*$		Gene 102, 171-178, 1991 A;Title: The porcine tumor necrosis factor-encoding genes: sequence and comparative analy A;Title: The porcine tumor in 17289 A;Accession: S17289 A;Accession: S17289 A;Accession: S17289 A;Residues: 1-204 <xuh></xuh>
the number of r than or equal ed by analysis	results predicted by chance to have a to the score of the result being printed, of the total score distribution. SUMMARIES	A, Cross-references: UNIPROT: P26445; EMBL: X54859; NID: 92132; PIDN: CAA38638.1; PID: 92133 C, Genetics: 32/3; 68/1 A; Introns: 32/3; 68/1 C; Superfamily: tumor necrosis factor C; Superfamily: tumor necrosis factor C; Keywords: cytokine; cytotoxin; glycoprotein; lymphokine; macrophage F;1-33/Domain: signal sequence #status predicted <sigs< td=""></sigs<>
Query Score Match Length DB ID	Description	F:54-204/FICOUCT: tumor necrosis ractor beta #status predicted <mai> Query Match 10.5%; Score 134.5; DB 1; Length 204;</mai>
5 204	tumor necrosis	<pre>imilarity 24.7%; Pred. conservative 31; Mis</pre>
10.1 232 1	tumor necrosis	SSPNSKN
10.1 235 Z 9.9 204 1 9.8 234 1	190 tumor necrosis fac 1ymphotoxin - bovi 141 tumor necrosis fac	DD 42 SAAQPAHQH-PPKHLARGTLKPAAHLVGDPSTPDSLRWRANTDRAFLR 88
9.6 233 1	tumor necrosi	Qy 116 WESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKY 175
9.5 205 1 9.4 235 1	IX lymphotoxin alpha tumor necrosis fac	Db 89LSNNSLLVPTSGLYFVXSQVVFSGEGCFPKATPTPLYLAHEVQLF 137
9.4 235 2	tumor necrosis	KALIMMAT TITAMWANIA TARAKA TARAKA INA TARAKA INA MANAKA MA
9.1 234 1	tumor necrosis	: : : : : : : : :
9.0 193 2 8.9 202 1	tumor necrosis	138
8.8 185 2 8.8 233 1	tumor necrosis tumor necrosis	235 SFFGAF
8.7 202 1 8.3 197 1	tumor necrosis tumor necrosis	Db 197 VFFGAF 202
7.7 233 2 6.3 203 2	tumor necrosis hypothetical pr	RESULT 2
6.1 202 2		A25451 tumor necrosis factor albha precursor - rabbit
5.9 195 2	peptide tran	
5.7 201 2	hypothetical pro	C;Decise: 0.7.003gus Cunicatus (Composit Labit) C;Darces:00-36p-1999 #sequence revision 10-5ep-1999 #text_change 09-Jul-2004
227 2 B704 112 2 AF03	hypothetical conserved hyp	Kiyota, T.; Hayashi,
5.6 123 2 T268	62	A;Title: Molecular cloning and expression in Escherichia coli of the cDNA coding for rabk

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crosis factor-encoding.genes: sequence and comparative anal, UID:91340150; PMID:1874444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKY 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ecursor - pig
ca (domestic pig)
_revision 10-Sep-1999 #text_change 09-Jul-2004
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tin; glycoprotein; lymphokine; macrophage
e #status predicted <SIG>
osis factor beta #status predicted <MAT>
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H64336
H21543
T21543
C317839
C317839
D90593
H81292
JE0351
S53800
B9189
T28300
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    72
         30
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A; Molecule type: mRNA A; Residues: 1-234 <ITO>

A;Accession: A25454

A; Accession: A25451 A; Molecule type: DNA

us-10-662-431-2_copy_39_

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A;Cross-references: EMBL:X54859; NID:g2132; PIDN:CAA38639.1; PID:g2134
A;Note: the authors translated the codon GAG for residue 202 as Gly
R;Choi, C.S.; Molitor, T.W.; Lin, G.F.; Murtaugh, M.P.
submitted to the EMBL Data Library, January 1991
A;Description: Complete nucleotide sequence of a cDNA encoding porcine tumor necrosis fac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C.Superfamily: tumor necrosis factor
C.Superfamily: tumor necrosis factor
C.Superfamily: tumor necrosis, glycoprotein; lipoprotein; lymphokine; macrophage; myris
F;1-7/Domain: propeptide #status predicted <PRO>
F;78-232/Product: tumor necrosis factor alpha #status predicted <MAT>
F;19-20/Binding site: myristate (Lys) (covalent) #status predicted
F;81/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;144-176/Disulfide bonds: #status predicted
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Immunogenetics 35, 351-353, 1995
A;Title: Sequence of the tumor necrosis factor/cachectin (TNF) gene from Peromyscus leucc
A;Reference number: 154490; MUID:92218012; PMID:1348497
                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:X57321; NID:g2137; PIDN:CAA40591.1; PID:g2138
R;Pauli, U.; Beutler, B.; Peterhans, E.
Rene Bi, 185-191, 1989
A;Title: Porcine tumor necrosis factor alpha: Cloning with the polymerase chain reaction A;Reference number: 146659; MUID:90034181; PMID:2478420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:P36939; GB:M59233; NID:g202506; PIDN:AAA40596.1; PID:g202507
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          137 VIHEKGFYYIYSQTYFRFQEEIKEN---TKNDKOMVQYIYKYTSYPDPILLMKSARNSCW 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124 VVPTDGLYLIYSQVLFRGQGCPSTNVFLTHTISRIA-----VSYQTKVNLLSAIKSPCQ 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66 GPLSINPLAQGLRSSSQTSDKPVAHVVANVKAEGQL--QWQSGYANALLANGVKLKDNQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tumor necrosis factor alpha precursor - white-footed mouse
C;Species: Peromyscus leucopus (white-footed mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
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C; Superfamily: tumor necrosis factor
C; Keywords: glycoprotein; lipoprotein; myristylation
F; 19,20/Binding site: myxistate (Lys) (covalent) #status predicted
F; 84/Binding site: carbohydrate (Ser) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Accession: 146659
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 44-232 cPAU>
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A;Molecule type: DNA
A;Residues: 1-235 <RES>
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Best Local Similarity
Matches 43; Conserva
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ses 45; Conserv
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A; Residues: 1-232 < CHO>
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A;Molecule type: DNA
A;Molecule type: 1-2, '0', 63-234 cSHA>
A;Molecule type: 1-34, Molecule type: 1-34, Molecul
                                                                                                                                                                    A;Cross-references: UNIPROT: P04924; GB:M12845; NID:g165759; PIDN:AAA31486.1; PID:g165766 R;Ito, H.; Shirai, T.; Yamamoto, S.; Akira, M.; Kawahara, S.; Todd, C.W.; Wallace, R.B. MNA S, 157-165, 1986 A;M. E. B. B. B. A;M. E. B. B. B. B. A;M. E. Molecular cloning of the gene encoding rabbit tumor necrosis factor. A;Reference number: A25451; MUID:86219712; PMID:3519138
                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-232 < CDRE>
A; Residues: 1-232 < CDRE>
A; Crose=references: UNIPROT: P23563; EMBL: X54001; NID: 92135; PIDN: CAA37949.1; PID: 92136
A; Crose=references: UNIPROT: P23563; EMBL: X54001; NID: 92135; PIDN: CAA37949.1; PID: 92136
B; Kuhnert, P.; Wuethrich, C.; Peterhans, E.; Pauli, U.
Gene 102, 171-178, 1991
A; Title: The porcine tumor necrosis factor-encoding genes: sequence and comparative anala; A; Reference number: S17289; MUD: 91340150; PMID: 1874444
A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            148 SQTYFRFQEEIKENTKNDKQMVQYIYKY-TSYPDPILLMKSARNSCWSKDAEYG----L 201
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Cispecies: Sus scrofa domestica (domestic pig)
Cispecies: Ju-Sep-1999 #sequence_revision lo-Sep-1999 #text_change (Cispacestion: S12606, S17290; S18965; 146659
Riprews, R.T.; Coffee, B.W.; Prestwood, A.K.; McGraw, R.A.
Nucleic Acids Res. 18, 5564, 1990
Arithe: Gene sequence of porcine tumor necrosis factor alpha.
A:Reference number: S12606; MUID:91016861; PMID:2216741
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A; Reference number: A25454; MUID:86219711; PMID:3519137
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220 VSVTNEHLIDMDHEAS-FFG 238
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A;Residues: 1-62,'S',64-233 <WAN>
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Matches 45; Conserv
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R;Su, X.; Morris, D.D.; McGraw, R.A.
Gene 107, 319-321, 1991
A;Title: Cloning and characterization of gene TNF alpha encoding equine tumor necrosis A;Reference number: JQ1344; MUID:92084125; PMID:1748301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cispecies: Bos primigenius taurus (cattle)
Cibate: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
Cibate: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
CiAccession: 1466045; 234641
RiCludts, I.; Cleuter, Y.; Kettmann, R.; Burny, A.; Droogmans, L.
Cytokine 5, 336-341, 1993
A;Title: Cloning and characterization of the tandemly arranged bovine lymphotoxin and A;Reference number: 146046; MUID:94083525; PMID:8260599
A;Accession: 146046
A;Status: preliminary; translated from GB/BMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-204 <CL2>
A;Cross-references: UNIPROT:Q06600; EMBL:Z14137; NID:g796; PIDN:CAA78510.1; PID:g797
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                         182 ILLMKSARNSCWSKDAEYG-----LYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEAS 235
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                                                                                                                                                    124 SFLSN-LHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKY-TSYPDP 181
                                                                                                                                                                                                                                                                                                                                                             61 TISTVQEKQQNISPLVRERGPQRVAAHITG-----TRGRSNTLSSPNSKNEKALGRKI 113
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NiAlternate names: cachectin; TNP alpha
C.Species: Equus caballus (domestic horse)
C.Species: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
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ISPLVRERGPQRVAAHITGTRGRSNTL-SSPNSKNEKALGRKINSWE---
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C;Superfamily: tumor necrosis factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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Best Local Similarity
Matches 47; Conserv
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A; Residues: 1-234 <SUX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        236 -FFG 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      228 VYFG 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lymphotoxin - bovine
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NiAlternate names: cachecin; TNPA
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: S-Aug-1985 #sequence revision 28-Aug-1985 #text change 09-Jul-2004
C;Accession: A3585; S36153; A39351; A44189; B61478; I53311; S62610; I14522; A01646; B23;
R;Nedwin, G.E.; Naylor, S.L.; Sakaguchi, A.Y.; Smith, D.; Jarrett-Nedwin, J.; Pennica, D.
Nucleic Acids Ree. 13, S361-6373, 1985
A;Fitle: Human lymphotoxin and tumor necrosis factor genes: structure, homology and chrom
A;Reference number: A93585; MUID:86016093; PMID:2995927
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R;Iris, F.J.M.; Bougueleret, L.; Prieur, S.; Caterina, D.; Primas, G.; Perrot, V.; Jurka, Nature Genet. 3, 137-145, 1993
A;Tile: Dense Alu clustering and a potential new member of the NFkappaB family within a A;Reference number: S36152; MUID:93272029; PMID:849947
A;Accession: S36152; MUID:93272029; PMID:8499947
A;Accession: S36152; MUID:9372029; PMID:8499947
A;Accession: S36152
A;Accession: S36153
A;Accession: Carlo Carl
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A;Molecule type: mRNA
A;Residues: 1-233 <PEN>
A;Residues: 1-233 <PEN>
A;Residues: 1-233 <PEN>
A;Residues: 1-233 <PEN>
A;Cross-references: GB:X02910; GB:X02159; NID:g37209; PIDN:CAA26669.1; PID:g37210
A;Cross-references: GB:X02910; GB:X02159; NID:g37209; PIDN:CAA26669.1; PID:g37210
A;Cross-references: GB:X02910; GB:X02159; NB:; Lin, L.S.; Strickler, J.; Van Arsdell, J.N.; Science 228, 149-154, 1985, A;Title: Molecular cloning of the complementary DNA for human tumor necrosis factor.
A;Reference number: A44189; MUID:85142190; PMID:3856324
C;Comment: This protein is an important proximal mediator of endotoxemia.
C;Genetics:
A;Gene: TFF-alpha
A;Gene: TFF-alpha
A;Introns: 62/3; 79/1; 95/1
C;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; memb; F;78-234/Product: tumor necrosis factor alpha #status predicted <TUM>
F;78-234/Product: tumor necrosis factor alpha #status predicted <TUM>
F;98-2018inding site: myristate (Lys) (covalent) #status predicted
F;82/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;82/Binding site: predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 ISTVQEKQ-----QNISPLVR-----ERGP-QRVAAHITGTRGRSNTLSSPNSKNEKALG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9.8%; Score 126; DB 1;
22.5%; Pred. No. 0.0025;
iive 35; Mismatches 72;
                                                                          ---SSRSGH 123
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--DAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDH 232

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178 YPDPILLMKSARNSCWSK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                        lymphotoxin alpha precursor
                                                                                                                                                                                               233 EAS-FFG 238
                                                                                                                                                                                                                                                                     223 SGQVYFG 229
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Ricross-references: GB:S68530; NID:g544751
Ricross-references: GB:S68530; NID:g544751
Ricrosson, F.T.; Bursten, S.L.; Locksley, R.M.; Lovett, D.H.
A; Exp. Med. 176, 1053-1062, 1092
A; Title: Myristyl acylation of the tumor necrosis factor alpha precursor on specific lysty.
A; Reference number: A59163; MUID:93018820; PMID:1402651
A; Contents: annotation; identification of myristylated lysines
A; Rogarwal, B.B.; Kohr, W.J.; Hass, P.E.; Moffat, B.; Spencer, S.A.; Henzel, W.J.; Bring J. Shol. Chem. 260, 2345-2354, 1985
A; Title: Human tumor necrosis factor. Production, purification, and characterization.
A; Reference number: A92511; MUID:85130974; PMID:3871770
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F;1-76/Domain: propeptide #status predicted <PRO>
F;77-233/Product: tumor necrosis factor #status experimental <MAT>
F;19,20/Binding site: myristate (Lys) (covalent) #status experimental
F;81/Binding site: carbohydrate (Ser) (covalent) (partial) #status experimental
F;145-177/Disulfide bonds: #status experimental
                                                                                                                                                                                                                      A; Molecule type: protein A; Residues: 83-102;109-119;121-128, X, X, 130-131;142-144, X, 146, XXXX, 150-152;159-174;186 M; Marmenout, A; Fransen, L; Tavernier, J; Van Der Heyden, J; Tizard, R.; Kawashima, Bur. J. Biochem. 152, 515-522, 1985
A; Title: Molecular cloning and expression of human tumor necrosis factor and comparison A; Reference number: IS3311; MUID:86030296; PMID:3932069
A;Cross-references: GB:M10988; NID:g339737; PIDN:AAA61198.1; PID:g339738
R;Fukuda, S.; Ando, S.; Sanou, O.; Taniai, M.; Fujii, M.; Masaki, N.; Nakamura, K.I.; An Lymphokine Res. 7, 175-185, 198
A;Title: Simultaneous production of natural human tumor necrosis factor-alpha, -beta and A;Reference number: A61478; MUID:88301617; PMID:2841543
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C; Comment: Secreted from mitogen-activated macrophages within 4-24 hours after induction
C; Comment: Secreted from mitogen-activated macrophages within 4-24 hours after induction
C; Comment: TNF-alpha and -bla (lymphotoxin) are the products of different genes closely
ut are produced by different cell types and have different induction kinetics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: A polymorphic variation in a putative regulation box of the TNFA promoter regid
A;Reference number: I54522; MUID:94102809; PMID:7903959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    œ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-233 «MAR»
A;Cross-references: GB:M26331; NID:g339763; PIDN:AAA36758.1; PID:g339764
A;Experimental source: U-937 cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Takakura-Yamamoto, R.; Yamamoto, S.; Fukuda, S.; Kurimoto, Bur. J. Biochem. 235, 431-437, 1996
A;Title: O-Glycosylated species of natural human tumor-necros
A;Reference number: 862610; MUID:96202967; PMID:8631363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA
A;Residues: 1-8 <DAL>
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A;Map position: 6p21.3-6p21.3
A;Introns: 62/3; 78/1; 94/1
C;Complex: homotrimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "D'Alfonso, S.; Richiardi, P.M. mmunogenetics 39, 150-154, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Molecule type: protein
Residues: 77-99 <TAK>
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A;Molecule type: mRNA
A;Residues: 1-59, N' 61-205 <KOB>
A;Cross-references: GB:D00102; NID:g219913; PIDN:BAA00064.1; PID:g219914
A;Note: the authors translated the codon TAT for residue 156 as Thr and ACC for residue 1
R;Fukuda, S.; Ando, S.; Sanou, O.; Taniai, M.; Fujii, M.; Masaki, N.; Nakamura, K.I.; Anc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NiAlternate names: Incombotoxin XIIIP beta; tumor necrosis factor beta (TNF beta)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: A92755; S36154; I54402; A93350; B32877; A91506; A61478; S26951; A01645; A23;
R;Nedwin, G.E.; Jarrett-Nedwin, J.; Smith, D.H.; Naylor, S.L.; Sakaguchi, A.Y.; Goeddel, J.; Cell. Blochem. 29, 171-181, 1985
A;Fitle: Structure and chromosomal localization of the human lymphotoxin gene.
A;Reference number: A92755; MUID:86086150; PMID:3001109
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A;Status: translation not shown; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-124, P',126-205 <RES>
A;Cross-references: GB:M55913; NID:9339742; PIDN:AAB59455.1; PID:9339743
A;Experimental source: ancestral haplotype 57.1
A;Note: 59-Asn was also found (ancestral haplotype 8.1)
B;Gray, P.W.; Aggarwal, B.B.; Benton, C.V.; Bringman, T.S.; Henzel, W.J.; Jarrett, J.A.;
Nature 312, 721-724, 1984
A;Fitle: Cloning and expression of cDNA for human lymphotoxin, a lymphokine with tumour r
A;Reference number: A93350; MUID:85086243; PMID:6334807
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A;Title: Dense Alu clustering and a potential new member of the NPkappaB family within a A;Reference number: S36152; MUID:93272029; PMID:8499947
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R;Goeddel, D.V.; Aggarwal, B.B.; Gray, P.W.; Leung, D.W.; Nedwin, G.E.; Palladino, M.A.;
Cold Spring Harb. Symp. Quant. Biol. 51, 597-609, 1986
A;Itle: Tumor necrosis factors: gene structure and biological activities.
A;Reference number: A32877; MUID:87217059; PMID:3472740
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A;Residues: 1-12,'R'.14-205 < IRI>
A;Cross-references: EMBL:215026; NID:937211; PIDN:CAA78746.1; PID:937213
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1992
R;Abraham, L.J.; Du, D.C.; Zahedi, K.; Dawkins, R.L.; Whitehead, A.S.
Immunogenetics 33, 50-53, 1991
A;Molecule type: mRNA
A;Residues: 1-205 <GRA>
A;Cross-references: GB:X01393; NID:g3444; PIDN:CAA25649.1; PID:g34445
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A;Residues: 35-205 <GOE>
K;Kobayaehi, Y.; Miyamoto, D.; Asada, M.; Obinata, M.; Osawa,
J. Biochem. 100, 727-733, 1986
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A;Reference number: I54482; MUID:91139175; PMID:1671667
A;Accession: I54482
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A;Residues: 1-59,'N',61-205 <NED>
A;Cross-references: UNIPROT:P01374
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A Introns: 62/3; 81/1; 97/1
A;Note: the first intron occurs in the 5'-untranslated region
C;Superfamily: tumor necrosis factor
C;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytokonin; glycoprotein; lipoprotein; lymphokine; macrophage; memb: F;80-235/Product: tumor necrosis factor #status experimental <MAT>
F;80-235/Product: tumor necrosis factor #status experimental <MAT>
F;84/Binding site: myristate (Lys) (covalent) #status predicted
F;86/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;86/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;86/Binding site: macrosis #status predicted
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R;Pennica, D.; Hayflick, J.S.; Bringman, T.S.; Palladino, M.A.; Goeddel, D.V.
Proc. Natl. Acad. Sci. U.S.A. 82; 6060-6064, 1985
A;Title: Cloning and expression in Escherichia coli of the cDNA for murine tumor necrosis
A;Reference number: A25164; MUID:85298296; PMID:3898078
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A; Residues: 1-235 <PEN>
A; Crossidues: 1-235 <PEN>
A; Crossidues: 1-235 <PEN>
A; Crossidues: 1-235 <PEN>
A; Fransen, L.; Muller, R.; Marmenout, A.; Tavernier, J.; van der Heyden, J.; Kawashima, F
Nucleic Acids Res. 13, 4417-4429, 1985
A; Fittle: Molecular cloning of mouse tumour necrosis factor cDNA and its eukaryotic expres
A; Reference number: A23127; MUID:85242112; PMID:2989794
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- Biol. Chem. 264, 16256-16260, 1989
A;Title: Chem. 264, 16256-16260, the cachectin/tumor necrosis factor propeptide results 3
A;Titles Alternative Cleavage of the cachectin/tumor necrosis factor propeptide results 3
A;Reference number: A34251; MUID:89380231; PMID:2777790
                                                                                                                                                                                                                                                                                   A.Title: Nucleotide sequence of the murine TNF locus, including the TNF-alpha-(tumor necal). Reference number: A93679; MUID:88067722; PMID:3684584
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A;Residues: 70-87 <CSE>
R;Caput, D.; Beutler, B.; Hartog, K.; Thayer, R.; Brown-Shimer, S.L.; Cerami, A.
Proc. Natl. Acad. Sci. U.S.A. 83, 1670-1674, 1986
A;Title: Identification of a common nucleotide sequence in the 3'-untranslated region of A;Reference number: I59058; MUID:86149365; PMID:2419912
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                                                                                                 A;Cross-references: GB:M38296; NID:g202086; PIDN:AAA40459.1; PID:g202087
A;Note: article in Russian with English abstract
R;Semon, D; Kawashima, E; Jongeneel, C.V.; Shakhov, A.N.; Nedospasov, S.A.
Nucleic Acids Res. 15, 9083-9084, 1987
A;Title: Nucleotide sequence of the murine TNF locus, including the TNF-alph
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A;Residues: 1-235 <FRA>
A;Cross-references: GB:X02611; NID:g54844; PIDN:CAA26457.1; PID:g54845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 235;
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23.1%; Pred. No. 0.0066;
ive 34; Mismatches 79; Indels
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A,Residues: 80-85,'X',87-99 <SHE>
C,Genetics:
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A, Residues: 1-235 <SEM>
                                                      1-235 <SHA>
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A;Reaidues: 1-235 <SH15
A;Createrences: UNIPROT:P06804; GB:M20155
A;Shakhov, A.N.; Nedospasov, S.A.
Bioorg. Khim. 13, 701-705, 1987
A;Title: Molecular cloning of the genes coding for tumor necrosis factors: complete nucl
A;Reference number: 503791; MUID:87298639; PMID:3040015
A;Accession: S03791
Lymphokine Res. 7, 175-185, 1988
A;Title: Simultaneous production of natural human tumor necrosis factor-alpha, -beta and
A;Reference number: A61478; MUID:88301617; PMID:2841543
                                                                                                                                                                                                       A;Molecule type: protein
A;Residues: 56-79;86-95, X', 97, 'X', 99;119-151, 'XX', 154-162, 'X', 164, 'X', 166, 'X', 168, 'X', 1
A;Residues: 56-79;86-95, X', 97, 'X', 99;119-151, 'XX', 154-162, 'X', 164, 'X', 166, 'X', 168, 'X', 1
A;Noigt. C.G.; Maurer-Pegy, I.; Adolf, G.R.
FEBS Lett. 314, 85-88, 1992
A;Title: Natural human tumor necrosis factor beta (lymphotoxin). Variable O-glycosylatic A;Reference number: $26951; MUID:93083656; PMID:1451807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Pukushima, K.; Watenabe, H.; Takeo, K.; Nomura, M.; Asahi, T.; Yamashita, K.
Arch. Blochem. Blophys. 304, 144-153, 1993
A;Title: N-linked sugar chain structure of recombinant human lymphotoxin produced by CHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Comment: Secreted from mitogen-activated lymphocytes within 1-2 days after induction, while having no detrimental effect on normal cells. It can also act synergistically wit C;Comment: This protein and TNF-alpha (tumor necrosis factor) are the products of differal activities but are produced by different cell types and have different induction ki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of the gene for mouse tumor necrosis
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C;Keywords: cytokine; cytotoxin; glycoprotein; homotrimer; lymphokine; macrophage
F:1-34/Domain: slignal sequence #status predicted <SIG>
F:35-205/Product: lymphotoxin #status predicted <MAT>
F;41/Binding site: carbohydrate (Thr) (covalent) (partial) #status experimental
F;96/Binding site: carbohydrate (Asn) (covalent) #status experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tumor necrosis factor alpha precursor - mouse
NiAlternate names: cachectin; TNF alpha
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 09-Jul-2004
C;Accession: A22908; S03791; Ā27303; A25164; A23127; A34251; IS9058; A36696
B;Shirai, T.; Shimizu, N.; Shiojiri, S.; Horiguchi, S.; Ito, H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Note: the first intron occurs before the initiator codon
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A;Reference number: A22908; MUID:88224564; PMID:2836146
A;Accession: A22908
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A,Cross-references: GDB:120442; OMIM:153440
A,Map Dostition: 6p21.3-6p21.3
A;Introns: 33/3; 69/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: protein
A;Residues: 35-59,'N', 61-205 <VOI>A;Note: 60-Thr was also found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Contents: annotation
                                                                                                                                                                  A; Accession: A61478
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R;Estler, H.C.; Grewe, M.; Gaussling, R.; Pavlovic, M.; Decker, K.
Biol. Chem. Hoppe-Seyler 373, 271-281, 1992
A;Title: Rat Lumor necrosis factor-alpha. Transcription in rat Kupffer cells and in vitz A;Reference number: S21674; MUID:92329007; PMID:1627266
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A; Residues: 17-235 <SHI>
A; Cross-references: UNIPROT:P16599
R; Kwon, J; Chung, I.Y; Benveniste, E.N.
Gene 132, 227-236, 1993
A; Title: Cloning and sequence analysis of the rat tumor necrosis factor-encoding genes.
A; Reference number: JN0868; MUID:94040766; PMID:8224868
                                                                                                                                                                                                                                                                                              N'Alternate names: cachectin; TNF alpha
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-Jun-1990 #sequence revision 07-Jun-1990 #text_change 09-Jul-2004
C;Accession: JU0029; JN0868; $21674
R;Shirai, T.; Shimiau, N.; Horiquchi, S.; Ito, H.
Agric. Biol. Chem. 53, 1733-1736, 1989
A;Title: Cloning and expression in Bscherichia coli of the gene for rat tumor necrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Accession: S21674
A;Molecule type: mRNA
A;Residues: 1-38, P',0-162,'T',164-201,'S',203-235 <EST>
A;Residues: 1-38,'P',0-162,'T',164-201,'S',203-235 <EST>
C;Coss-references: GB:X66539; GB:S40199; NID:g395369; PIDN:CAA47146.1; PID:g395370
C;Comment: Tumor necrosis factor is secreted by macrophages in response to endotoxin
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                            66 QEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSP-----NSKNEKALGRKINSWESS 119
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---LYSIYQGGIFELKENDRIFVSVTNEHLIDMDHE 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Introns: 62/3; 81/1; 97/1
C;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine;
F;80-235/Product: tumor necrosis factor #status predicted «MAT»
F;19,20/Binding site: myristate (Lys) (covalent) #status predicted
F;84/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;86/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9.4%; Score 121; DB 2; 23.0%; Pred. No. 0.0066;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DPILLMKSARNSCWSKDAEYG---
                                                                                                                                                                                                                                                                              tumor necrosis factor alpha precursor
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A;Accession: JU0029
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225 SGQVYFG 231
                                                                                                234 AS-FFG 238
                                                                                                                                               GOVYFG 231
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Best Local Similarity
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A; Residues: 1-235 < KWO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A, Molecule type: DNA
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180
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A;Cross-references: UNIPROT:P33620; EMBL:X62141; NID:938159; PIDN:CAA44068.1; PID:938160
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C;Species: Ovis cachectin; TNF alpha
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Accession: JH0529; 848118; 513114; S20661
R;Green, I.R.; Sargan, D.R.
R;Green, I.R.; Sargan, D.R.
A;Title: Sequence of the cDNA encoding ovine tumor necrosis factor-alpha: problems with A;Reference number: JH0529; MUID:92112044; PMID:1765267
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A; Residues: 1-24 <GRES.
A; Cross-references: UNIPROT: P23383; EMBL: X55152; NID: g1405; PIDN: CAA38952.1; PID: g1406
A; Experimental source: alveolar macrophage
A; Nash, Ab.; Barcham, G.J.; Brandon, M.R.; Andrews, A.E.
Immunol. Cell Biol. 69, 273-283, 1991
A; Title: Molecular cloning, expression and characterization of ovine TNF-alpha.
A; Reference number: 848118; MUID: 92155784; PMID: 1786996
                                                                                                                RiSanjanwala, M.; Edwards, A.
RiSanjanwala, M.; Edwards, A.
A;Description: Baboon Tumor Necrosis Factor Derived from Sequences of Genomic DNA.
A;Reference number: S22052
A;Accession: S22052
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124 SFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYT----S 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        112 LLANGVELRDNQLVVPSEGLYLIYSQVLFKGQ-----GCPSTHVLLTHTISRIAVS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               178 YPDPILLIMKSARNSCWSK----DAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDH 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Papio sp. (baboon)
C;Date: 10-Sep.1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
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R;Young, A.J.; Hay, J.B.; Chan, J.Y.C.
Nucleic Acids Res. 18, 6723, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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A;Introns: 62/3; 78/1; 94/1

C;Superfamily: tumor necrosis factor

C;Keywords: glycoprotein; lipoprotein; myristylation; transmembrane

F;19,20/Binding site: myristate (Lys) (covalent) #status predicted

F;81/Binding site: carbohydrate (Ser) (covalent) #status predicted

F;145-177/Disulfide bonds: #status predicted
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Pred. No. 0.008;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 9.3%; Score 120; DB Best Local Similarity 23.0%; Pred. No. 0.00 Matches 43; Conservative 32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tumor necrosis factor alpha precursor
necrosis factor alpha
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                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-233 <SAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A, Molecule type: mRNA
A, Residues: 1-234 <NAS>
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A; Status: preliminary
                                                                                                        C; Accession: $22052
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149 PWYEPIYQGGVFQLEKGDRLSABINQPEYLDYAESGQVYFG 189
                                                                                                                                                                                                                                     199 YGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEAS-FFG 238
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A;Title: Cloning and expression of murine lymphotoxin cDNA
A;Reference number: 155980; MUID:8724127; PMID:2884262
A;Accession: 155980
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A;Molecule type: DNA
A;Residues: 1-202 <RE2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tumor necrosis factor beta precursor - mc
N;Alternate names: lymphotoxin; TNF beta
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A, Residues: 1-25,'P',27-202 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 6-202 <WEI>
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                                                                                         A; Molecule type: mRNA
A; Residues: 1-62, 64-234 < YOU>
A; Cross-references: EMBL:X5596; NID:g1403; PIDN:CAA39437.1; PID:g1404
A; Note: comparison with the introns of homologous sequences suggest that this is probabl
C; Superfamily: tumor necrosis factor
C; Reymorts: alternative splicing; cytotoxin; glycoprotein; lipoprotein; lymphc
F; 1-77/Domain: propeptide #status predicted < FNO>
F; 20/Binding site: myristate (Lys) (covalent) #status predicted
F; 82/Binding site: carbohydrate (Ser) (covalent) #status predicted
F; 96/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A;Residues: 36-38,'S',40-78,'A',80-88,'N',90-114,'Q',116-123,'D',125-144,'G',145-173,'L'
A;Residues: 36-38,'S',40-78,'A',80-88,'N',90-114,'Q',116-123,'D',125-144,'G',145-173,'L'
A;Cross-references: EMBL:X77317; NID:g452607; PIDN:CAA54523.1; PID:g452608
C;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytokoxin; glycoprotein; lymphokine; macrophage; membrane protein
F;42/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;106-138/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;Molecule type: mRNA
;Residues: 1-193 <GOL>
;Cross-references: UNIPROT:P13296; EMBL:X14828; NID:g992; PIDN:CAA32937.1; PID:g993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      128 NLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYT-----SYPDP 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           168 VNILSAIKSPCHRETLEGAEAKPWYEPIYOGGVFOLEKGDRLSABINLPEYLDYAESGOV 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFYYIYS 148
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N;Alternate names: cachectin; TNF alpha
C;Species: Capra aegagrus hircus (domestic goat)
C;Species: Capre-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
C;Accession: S06192; 841867
R;Goldstein, I.M.; Henner, D.; Talhouk, A.
submitted to the EMBL Data Library, March 1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        182 ILLAMKSARNSCWSK----DAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEAS-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 9.1%; Score 117.5; DB 1; Length 234; Best Local Similarity 23.0%; Pred. No. 0.013; Matches 42; Conservative 30; Mismatches 78; Indels 33.
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      A; Reference number: $13114; MUID: 91067496; PMID: 2251151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19 PEEEQSPAGPSFN-----RPLVQ--TLRSSSQASS--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;146-178/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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A;Accession: S41867
A;Status: preliminary
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A,Residues: 1.202 - CSEM>
A;Cross-references: UNIPROT: P09225; GB:Y00467; NID:954830; PIDN:CAA68529.1; PID:954831
A;Cross-references: UNIPROT: P09225; GB:Y00467; NID:954830; PIDN:CAA68529.1; PID:954831
R;Nedospasov, S.A.; Hirt, B.; Shakhov, A.N.; Dobrynin, V.N.; Kawashima, B.; Accolla, R.S.
Nucleic Acids Res. 14, 7113-7725, 1986
A;Title: The genes for tumor necrosis factor (TNF-alpha) and lymphotoxin (TNF-beta) are t
A;Reference number: S01342; MUID:87040736; PMID:3490653
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R; Gardner, S.M.; Mock, B.A.; Hilgers, J.; Huppi, K.E.; Roeder, W.D.
J. Immunol. 139, 476-483, 1987
A; Title: Mouse lymphotoxin and tumor necrosis factor: Structural analysis of the cloned gas Reference number: 156004; MUD:8752204; PMID:2885372
A; Reference number: 156004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 10-5ep-1999 #sequence revision 10-5ep-1999 #text change 09-Jul-2004
C;Accession: B27303; S01342; S10083; I55004; I48853; I55590
R;Semon, D.; Kawashima, E.; Jongeneel, C.V.; Shakhov, A.N.; Nedospasov, S.A.
Nucleic Acids Res. 15, 9083-9084, 1987
A;Title: Nucleotide sequence of the murine TNF locus, including the TNF-alpha-(tumor nec: A;Reference number: A93679; MUID:88067722; PMID:3684584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: DNA
A;Residues: 1-11;139-160,'CG',163-178 <NED>
A;Cresidues: BMBL:X06217
A;Cresidi, D.; Dautry, F.
Oncogene Res. 3, 409-414, 1988
A;Title: Induction of tumor necrosis factor-alpha and -beta and interferon-gamma mRNA by
A;Reference number: $10083; WUID:89144562; PMID:3147435
                                                                 98 QVLFR------GHGCPSTPLFLTHTISRIAVSYQTKVNILSAIKSPCHRETPEAEAK 148
QTYFRFQEEIKENTKNDKQMVQYIYKYT----SYPDPILLMKSARNSCWSK----DAE
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Rimercens, B.; Gaidulis, L. submitted to the EMBL Data Library, March 1995 states consigned and sequence analysis of cDNAs encoding bovine CD40 ligand and bd A;Reference number: $52715 states preliminary a;Molecule type: mRNA a;Residues: 1-185 states and A;Residues: 1-185 states and A;Residues: 1-185 states and A;Residues: 1-185 states and A;Residues: Limor necrosis factor C;Superfamily: tumor necrosis factor C;Superfamily: tumor necrosis factor E;33/Binding site: carbohydrate (Ser) (covalent) #status predicted F;97-129/Disulfide bonds: #status predicted
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                                                                                                                                                                                                                                                                                   80 GPQRVAAHITGTRGRSWTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIH 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100 TSGLYFVYSÖVVFSGESCSPRAIPTPIYLAHEVQLFSSQYPFHVPLL-SAQKSVYPGLQG 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80 GPORVAAHITGTRGRS---NTL-SSPNSKNEKALGR---KINS----WESSRSGHSFLS 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               128 NLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYK--YTSYPDPILLM 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      186 KSARNSC-----WSKDAEYGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEAS-FFG 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 GPQREEQSPGGPSINSPLVQTLRSSSQASSNKPVAHVVADINSPGQLRWWDSYANALMAN 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tumor necrosis factor alpha precursor - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 04-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 8.8%; Score 113.5; DB 2; Length 185;
Best Local Similarity 25.0%; Pred. No. 0.021;
Matches 45; Conservative 29; Mismatches 79; Indels 27; Gaps
                                                                                                                                                                                                                         81; Indels 18; Gaps
A;Map position: 17
A;Introns: 32/3; 66/1
C;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytotoxin; glycoprotein; lymphokine; macrophage
                                                                                                                                                        Query Match 8.9%; Score 114; DB 1; Length 202; Best Local Similarity 23.5%; Pred. No. 0.021; Matches 38; Conservative 25; Mismatches 81; Indels in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         199 YGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
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Job time : 42 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

Run. on:

3, 2005, 06:15:49 ; Search time 40 Seconds (without alignments) 675.923 Million cell updates/sec

US-10-662-431-2 1478 Title: Perfect score:

1 MAMMEVQGGPSLGQTCVLIV.....NEHLIDMDHEASFFGAFLVG 281 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* **Database**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	G G		A53062
	9	1	N
	Length		279
Query	Match		12.8
	Score		189.5
Result	No.	1 1 1	н

	ption	Fas ligand - mouse	Fas ligand - human	ligand -	CD40 ligand - bovi	CD40 ligand - huma	tumor necrosis fac	CD40 ligand - mous	818		tumor necrosis fac	tumor necrosis fac		вів	Д			tumor necrosis fac	lymphotoxin alpha	BiB			tumor necrosis fac	lymphotoxin-beta -	д	tumor necrosis fac	amphotropic murine	tumor necrosis fac	lymphotoxin beta -	probable membrane
	ID	A53062	138707	A49266	853090	153476	A25451	S21738	S17289	S12606	\$22052	JQ1344	S24642	154490	S24641	OWHUN	OMMSN	JU0029	QWHUX	JH0529	806192	B27303	S52715	149139	QQBY2M	JN0869	I48083	JH0309	0	AB1658
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	Score	189.5	186	177.5	164	147.5	141	141	134.5	133	131.5	131	130.5	•	•	125.5	123.5	123.5	122	121	115.5	-		13.	112.5	111.5	109	107	102	100
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tumor necrosis fac	protein kinase, pr	DNA ligase homolog	hypothetical prote	hypothetical prote	hypothetical prote	chromodomain helic	heat shock transcr	cardiac muscle fac	myosin-light-chain	serine/threonine k	activin receptor-l	hypothetical prote	hypothetical prote	NBS-LRR type resis	alpha-N-arabinofur
S11688	F95122	T14707	T15010	G95104	T18489	T23056	A31593	T29095	JN0583	JC2491	A53444	T40578	E96636	T03031	B59296
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ALIGNMENTS

RESULT 1 A53062 Fas ligand - mouse C;Species: Mus musculus (house mouse) C;Species: Tanakaulus (house mouse) C;Accession: A53062 R;Takahashi, T:; Tanaka, M:; Brannan, C.I.; Jenkins, N.A.; Copeland, N.G.; Suda, T.; Naga A;Title: Generalized lymphoproliferative disease in mice, caused by a point mutation in t A;Reference number: A53062; MUID:94185175; PMID:7511063 A;Accession: A53062 A;Status: preliminary A;Molecule type: mRNA A;Redicues: L-779 < TRNA A;Redicues: L-770 < TRNA A;Redicues: L-770 < TRNA	Query Match 12.8%; Score 189.5; DB 2; Length 279; Best Local Similarity 25.8%; Pred. No. 1.7e-08; Matches 51; Conservative 50; Mismatches 64; Indels 33; Gaps 9;	QY 83 QLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSK 142	Qy 143 NEKALGRKINSWESSRSGHSFLSNLHLERNGELVIHEKGFYYIYSQTYFRFQEEIKENTKN 202 155 SIPLEWEDT-YGTALISGVKYKKGGLVINETGLYFVYSKVYFRGQSCN 201	Qy 203 DKQMVQYIY-KYTSYPDPILLMKSAR-NSCWSKDAEYGLYSIYQGGIFELKENDRIFVSV 260 :::: : : : : : : Db 202 NQPLNHKVYMRNSKYPEDLVLMEEKRLNYCTTGQIWAHSSYLGAVFNLTSADHLYVNI 259	Qy 261 TNEHLIDMDHEASFEGAF 278 1 : : : : Db 260 SQLSLINFEESKTFFGLY 277	RESULT 2
MAROUCURPARARA MAROUCURPARARA		& A	상 원	\$ A	S G	RE

CiSpecies: Homo sapiens (man)
CiAccession: I38707; UC2340; E57565; I38554
RiTakahashi, T.; Tanaka, M.; Inazawa, J.; Abe, T.; Suda, T.; Nagata, S.
Int. Immunol. 6, 1567-1574, 1994
A;Title: Human Fas ligand: gene structure, chromosomal location and species specificity.
A;Reference number: I38707; MUID:95127560; PMID:7826947
A;Reference number: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-281 cRES>
A;Cross-references: UNIPROT:P48023; EMBL:U11821; NID:9595430; PIDN:AAC50124.1; PID:959543

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50; Conservative
                                                Local Similarity
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                                                                                                                                                                                      Rischatzlein, C.E.

Submitted to the EMBL Data Library, June 1995

A; Reference number: $57565

A; Accession: $57565

A; Status: preliminary

A; Status: preliminary

A; Status: preliminary

A; Status: preliminary

A; Residues: 1-281 < SCH>
A; Cross-references: EMBL:X89102; NID:g887455; PID:g887456

A; Cross-references: EMBL:X99102; NID:g887455; PID:g887456

A; Title: Fas ligand mediates activation-induced cell death in human T lymphocytes.

A; Reference number: 138554; MUID:95105731; PMID:7528780
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R;Suda, T.; Takahashi, T.; Golstein, P.; Nagata, S.
R;Suda, T.; Takahashi, T.; Golstein, P.; Nagata, S.
A;Title: Molecular cloning and expression of the Fas ligand, a novel member of the tumor
A;Reference number: A49266; MUID:94084792; PMID:7505205
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Ç.Keywords: glycoprotein; transmembrane protein
                                                                                                                                                                    A,Cross-references: GB:D38122; DDBJ:D29820; NID:g601892; PIDN:BAA07320.1; PID:g1369902
E.; Hayashi, N.; Iio, S.; Takehara, T.; Hijioka, T.; Kasahara, A.; Fusamoto,
                 Biochem. Biophys. Res. Commun. 204, 468-474, 1994
A;Title: Role of Fas ligand in apoptosis induced by hepatitis C virus infection. A;Reference number: JC2340; MUID:95071350; PMID:7980502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Introns: 151/1; 116/3
C;Keywords: 91ycoprotesin; transmembrane protein
F;80-102/Domain: transmembrane #status predicted <TMM>
F;76,184,250,260/Binding aite: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           147 ---AHLT---GKSNSRSMP-----LEWEDT-YGIVLLSGVKYKKGGLVINETG 187
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 MEVOGGPSLGQTCVLIVIFTVLLQSLCVAV---TYVYFTNELKQMQDKYSKSGIACFLKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cross-references: EMBL:U08137; NID:g624627; PIDN:AAC50071.1; PID:g624628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82; Indels 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------KKELRKV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12.6%; Score 186; DB 2; 22.1%; Pred. No. 3.4e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Accession: 138554
A,Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 130 QIGHPSPPPE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                       A;Molecule type: DNA
A;Residues: 1-281 <MIT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-278 <SUD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-281 <RE2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Accession: A49266
                                                                                             A; Accession: JC2340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                234
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Best Local &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene: FasL
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T53476
CD40 ligand - human
NyAlternate names: glycoprotein 39; hCD40-L protein; T-cell antigen gp39; TRAP protein
NyAlternate names: glycoprotein 39; hCD40-L protein; T-cell antigen gp39; TRAP protein
NyAlternate names: glycoprotein (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence revision 02-Jul-1996 #text change 09-Jul-2004
C;Accession: S28017, JUN-93; S26694; S28852; I53476; S25684; S30593
C;Accession: S28017, JUN-93; Z26694; S28852; I53476; S25684; S30593
EMBO J. 11, 4313-4321, 1992
A;Title: The human T cell antigen gp39, a member of the TNF gene family, is a ligand for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
A;Molecule type: mENA
A;Residues: 1-261 <MER>
A;Cross-references: UNIPROT:P51749; EMBL:Z48469; NID:g732569; PIDN:CAA88363.1; PID:g73257
                                                                                                                                                100 ISTVQEKQQNISPLVRERGPQRVAAHITGT-RGRSNTLSSPNSKNEKALGRKINSWESSR 158
                                                                                                                                                                                                                                                                                                    159 SGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIY-KYTSYP 217
                                                                                                                                                                                                                                                                                                                                           -------EWEDT- 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                        DPILLAMKSAR-NSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFG 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117 GDLVLMEEKKLNYCTT--GQIWAHSSYLGAVFNLTVADHLYVNISQLSLINFEESKTFFG 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 YWDPNDEESMNS--PCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQR 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69 IQRCNKGEGSLSLINCEEIRSRFEDLV-KDIMQNKE-----VKKKEKNFEMHKGDQEPQ- 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 VAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSN--LHLRNG-ELVIHE 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  179 KGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYG 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              166 QGFYYIYTQVTFCSNRE----TLSQAPFIASLCLKSPSGSERILLRAANTHSSSKPC--G 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 VQGGPSLGQTCVLIVIFTVLL--QSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKEDDS 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Bos primigenius taurus (cattle)
C;Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C;Accession: S53090
C;Accession: S53090
A;Becerore number: S53090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13 VATGPPVSMK-IFMYLLTVFLTTQMIGSALFAVYLHRRLDKIEDERNLHEDFVFMK---T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40;
Length 278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52; Mismatches 114; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           239 LYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFG 276
   DB 2;
                                                                                                                                                                                                                      121 VSSFEKQIANPSTPSETKKPRSV-AHLTGNPRSRSIPL-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 11.1%; Score 164; DB 2; Best Local Similarity 25.9%; Pred. No. 2.3e-06; Matches 72; Conservative 52; Mismatches 114
                                   .8e-07;
12.0%; Score 177.5;
27.5%; Pred. No. 1.8e
ive 39; Mismatches
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CD40 ligand - mouse
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Best Local S:
Matches 62
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                                                                                              A, Residues: 1-261 <HOL>
A, Residues: 1-261 <HOL>
A, Roberterences: UNIPROT: P29965; EMBL: Z15017; NID: 938483; PIDN: CAA78737.1; PID: 938484
R, Spriggs, M.K.; Armitage, R.J.; Strockbine, L.; Clifford, K.N.; Macduff, B.M.; Sato, T.J. Exp. Med. 176, 1543-1550, 1992
A, Exp. Med. 176, 1543-1550, 1992
A, Title: Recombinant human CD40 ligand stimulates B cell proliferation and immunoglobuli A, Reference number: JH0793; MUID: 93084757; PMID: 1281209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-261 <GRA>
A;Cross-references: ENBL:X68550; NID:937269; PIDN:CAA48554.1; PID:937270
B;Gauchat, J.F.; Aubry, J.P.; Mazzei, G.; Life, P.; Jomotte, T.; Elson, G.; Bonnefoy, J. R;Gauchat, 315, 259-266, 1993
A;Title: Human CD40-ligand molecular cloning, cellular distribution and regulation of e A;Reference number: 828852; MUID:93138085; PMID:7678552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Wolecule type: mRNA
A;Residues: 1-261 cGNA
A;Cross-references: EMBL:L07414; NID:g180123; PIDN:AAA35662.1; PID:g180124
A;Note: the sequence from Fig. 3 is inconsistent with that from Fig. 2 in having 6-Gln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          129 TRGRSNTLSSPNSKWEKALGRKINSWESSRSGHSFLSN--LHLRNG-ELVIHEKGFYYIY 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 186 SQTYFRFQEEIKENT-----KNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEY 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 173 AQVTPCSNREASSQAPFIASLCLKSPGRFER-------ILLRAANTHSSAKPC-- 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 VLIVIFTVLL--QSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKEDDSYWDP----ND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23 IFMYLLTVFLITQMIGSALFAVYLHRRLDKIEDERN-----LHEDFVFMKTIQRCNTG
                                                                                                                                                                                                                                                                                                                                                                                        Cross-references: GB:X67878; NID:g38411; PIDN:CAA48077.1; PID:g38412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Cross-references: GDB:120632; OMIM:308230
A;Map position: XQ26-XQ26
C;Keywords: glycoprotein; transmembrane protein
F;13-44/Domain: transmembrane #status predicted <TMM>
F;6-261/Domain: extracellular #status predicted <EXT>
F;6,240/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10.0%; Score 147.5; DB 2; Length 261; 23.7%; Pred. No. 5.7e-05; Live 51; Mismatches 99; Indels 63
                                                                                                                                                                                                                                                                                                                                                                                                                   A; Experimental source: peripheral blood T-cell
R;Graf, D.; Korthaeuer, U.; Mages, H.W.; Senger, G.; Kroczek,
Eur. J. Immunol. 22, 3191-3194, 1992
A;Ttele: Cloning of TRAP, a ligand for CD40 on human T cells.
A;Reference number: S26694; MUID:93076854; PMID:1280226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFG 276
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A;Accession: S28017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Gene: GDB: CD40LG; HIGM1; IMD3
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nes 66; Conservative
                                                                   A;Molecule type: mRNA
A;Residues: 1-261 <HOL>
                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-261 <SPR>
                                                                                                                                                                                                                                                                                             A; Accession: JH0793
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Matches
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tumor necrosis factor alpha precursor - rabbit
N;Alternate names: cachectin; TNF alpha
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 10-Sep.1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A25454; A25451; JS0727

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R;Ito, H.; Yamamoto, S.; Kuroda, S.; Sakamoto, H.; Kajihara, J.; Kiyota, T.; Hayashi, H.; DNA 5, 149-156, 1986
A;Title: Molecular cloning and expression in Escherichia coli of the cDNA coding for rabk A;Title: Molecular number: A25454
A;Accession: A25454
A;Molecule type: mRNA
A;Residues: 1-234 <ITO>
A;Cross-references: UNIPROT:P04924; GB:MI2845; NID:g165759; PIDN:AAA31486.1; PID:g165760
B;Ito, H.; Shirai, T.; Yamamoto, S.; Akira, M.; Kawahara, S.; Todd, C.W.; Wallace, R.B.
DNA 5, 157-165, 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Molecule type: DNA
A,Robestides: 1-234 <1T2>
A,Robestides: 1-234 <1T2>
A,Robestides: 1-234 <1T2>
A,Note: this sequence differs from that shown in having a Gln inserted between residues (R,Shakhov, A.N.; Kuprash, D.V.; Azizov, M.M.; Jongeneel, C.V.; Nedospasov, S.A. Gene 95, 215-221, 1990
A,Fitle: Structural analysis of the rabbit TNF locus, containing the genes encoding TNF-?
A,Reference number: JH0309; MUID:91065534; PMID:2249779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A) Introductions: 62/3; 80/1; 96/1

C;Superfamily: tumor necrosis factor

C;Superfamily: tumor necrosis factor

C;Superfamily: tumor necrosis gradicted <PRO>

F;1-Bil/Domain: propeptide #status predicted <PRO>

F;82-234/Product: tumor necrosis factor #status predicted <MAT>

F;83-20/Eniding site: myristate (Lys) (covalent) #status predicted

F;83/Binding site: carbohydrate (Ser) (covalent) #status predicted

F;147-178/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
B
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C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: $21738
R;Armitage, R.J.; Fanslow, W.C.; Strockbine, L.; Sato, T.A.; Clifford, K.N.; Macduff, Cosman, D.; Spriggs, M.K.
Nature 357, 80-82, 1992
A;Title: Molecular and biological characterization of a murine ligand for CD40.
A;Reference number: $21738; MUID:92244364; PMID:1374165
A;Accession: $21738
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-62,'Q',63-224 <SHA> A;Cross-references: GB:M60340; GB:M35326; NID:g165754; PIDN:AAA31484.1; PID:g165756 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68 NDEESMNSPCWQVKWQLRQLVRKMI-LRTSEETISTVQEKQQNISPLVRERGPQRVAAHI 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  127 TGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFYYIYS 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QVLFSGQ-----GCRSYVLLTHTVSRFAVSYPNKVNLLSAIKSPCHRETPEBABPMAWYE 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95 VA-------NPQVEGQL-----QWLSQRANALLANGMKLTDNQLVVPADGLYLIYS 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Molecular cloning of the gene encoding rabbit tumor necrosis factor. A;Reference number: A25451; MUID:86219712; PMID:3519138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59 QEEESPINN-----LHLVNPVAQMVTLRSASRALSD------KPL-----AHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   187 QTYFRFQEEIKENTKUDKQMVQYIYKY-TSYPDPILLMKSARNSCWSKDAEYG----LY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 GGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKEDDSYMDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 9.5%; Score 141; DB 1; Length 234; I Similarity 22.4%; Pred. No. 0.00017; 62; Conservative 41; Mismatches 98; Indels 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  194 PIYLGGVFQLEKGDRLSTEVNQPEYLDLAESGQVYFG 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEAS-FFG 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22 GGPQGSKRCLCLSLFSFLL---VAGATTLF-
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55 --VIGPQKEEFPAGPL----
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A; Residues: 1-232 < CHO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: 146659
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A;Cross-references: UNIPROT:P27548; EMBL:X65453; NID:g50351; PIDN:CAA46448.1; PID:g50352 C;Keywords: glycoprotein; transmembrane protein C273-454 Domain: transmembrane #status predicted <TWM> F;23-450/Domain: extracellular #status predicted <TWM> F;47-260/Domain: extracellular #status predicted <EXTN> F;239/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               comparative anal
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A;Reaidues: 1-204 <KUH;
A;Cross-references: UNIPROT:P26445; EMBL:X54859; NID:g2132; PIDN:CAA38638.1; PID:g2133
C;Genetics:
                                                                                                                                                                                                                                                                                                                         11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CSNRE----PSSQRPFIVGLWLKPSIGSERILLLXAANTHSSSQLCEQ--QSVHLGGVFEL 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----HGFL----LSNNSLLVPTSGLYFVYSQVVFSGEGCFPKATPTPLYLAHEVQLF 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               133 SNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNL-HLRNG-ELVIHEKGFYYIYSQTYF 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             191 RFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFEL 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      101 STVQEKQQNISPLVRERGPQRVAAHITG-----TRGRSNTLSSPNSKNEKALGRKINS 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   214 TS-YPDPILLMKSARNSCWSKDABYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEA 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88
                                                                                                                                                                                                                                                                                                                                                                                                                                              tumor necrosis factor beta precursor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                              17 VLIVIFTVLL--QSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKEDDSYWDPNDEESMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S--PCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQRVAAHITGTRGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SLINCEEMRRQFEDLVKDITINK------EEKKENSFEMQRGDEDPQIAAHV----
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                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C,Accession: S17289 Logonico_Corporate Coperation of C,Accession: S17289 Coperation C,Accession: S1728 C,Acc
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                                                                                                                                                                                                                                                                                                                    38;
                                                                                                                                                                                                                                       9.5%; Score 141; DB 2; Length 260; larity 23.5%; Pred. No. 0.0002; Conservative 50; Mismatches 104; Indels
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QAGASVFVNVT 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   251 KENDRIFVSVT 261
                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 59; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      197 VFFGAF 202
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Julitons: 62/3; 78/1; 93/1

G'Superfamily: tumor necroosis factor

G'Superfamily: tumor necroosis factor

G'Reywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; myris

F;1-77/Domain: propeptide #status predicted <PRO>

F;18-232/Product: tumor necrosis factor alpha #status predicted

F;18-232/Product site: myristate (Lys) (covalent) #status predicted

F;81/Binding site: carbohydrate (Ser) (covalent) #status predicted

F;81/Binding site: carbohydrate (Ser) (covalent)
                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-212 - DNA
A; Residues: 1-212 - DNES-
A; Cross-references: UNIPROT: P23563; EMBL: X54001; NID: 92135; PIDN: CAA37949.1; PID: 92136
A; Kühnert, P.; Wuethrich, C.; Peterhans, E.; Pauli, U.
Gene 102, 171-178, 1991
A; Tille: The porcine tumor necrosis factor-encoding genes: sequence and comparative anal; A; Reference number: S17289; MUID: 91340150; PMID: 1874444
A; Reference number: S17289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-232 «KUH>
A; Cross-references: EMBL:X54859; NID:g2132; PIDN:CAA38639.1; PID:g2134
A; Cross-references: EMBL:X54859; NID:g2132; PIDN:CAA38639.1; PID:g2134
A; Note: the authors translated the codon GAG for residue 202 as Gly
R; Choi, C.S.; Molitor, T.W.; Lin, G.F.; Murtaugh, M.P.
submitted to the EMBL Data Library, January 1991
A; Description: Complete nucleotide sequence of a cDNA encoding porcine tumor necrosis factal statemer number: $18965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:X57321; NID:g2137; PIDN:CAA40591.1; PID:g2138
R;Pauli, U.; Beutler, B.; Peterhans, E.
Gene 81, 185-191, 1999
A;Title: Porcine tumor necrosis factor alpha: Cloning with the polymerase chain reaction
A;Reference number: 146659; MUID:90034181; PMID:2478420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76 -----GLRSSSQTSDKPVAHVVANVKAEGQL--QWQSGYANALLANGVKLKDNQLVVPT 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      128 DGLYLIYSQVLFRGGGCPSTNVFLTHTISRIA-----VSYQTKVNLLSAIKSPCQRETP 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
tumor necrosis factor alpha precursor - pig
C;Species: Sus scroff adomestica (domestic pig)
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
C;Dates: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S12606; S17290; S18965; 146659
R;Drews, R.T.; Coffee, Bw., Prestwood, A.K.; McGraw, R.A.
Nucleic Acids Res. 18, 554, 1990
A;Title: Gene sequence of portine tumor necrosis factor alpha.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    179 KGFYYIYSQTYFRFQEEIKEN---TKNDKQMVQYIYKYTSYPDPILLIMKSARNSCWSK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 AMMEVOGGPSLGOTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----SINPLAQ-----
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A,Residues: 44-232 <PAU>
A,Cross-references: GB:M29079; NID:g164694; PIDN:AAA31128.1; PID:g164695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 9.0%; Score 133; DB 1; Length 232; Best Local Similarity 21.3%; Pred. No. 0.00082; Matches 61; Conservative 40; Mismatches 100; Indels 8
                                                                                                                                                                                                                                                                                                                       A;Reference number: $12606; MUID:91016861; PMID:2216741
A;Accession: $12606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
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C.Species: Bos primigentus faurus (cattle)
C.Species: Bos primigentus taurus (cattle)
C.Date: 10-8p-1999 #sequence_revision 10-8ep-1999 #text_change 09-Jul-2004
C.Accession: I46047; S24642
R.Cludts, I.; Cleuter, Y.; Kettmann, R.; Burny, A.; Droogmans, L.
Cytokine 5, 336-341, 1993
A.Fitle: Cloning and characterization of the tandemly arranged bovine lymphotoxin and A, Reference number: I46046; MUID:94083525; PMID:8260599
A.Starro. ______
                                                                                                                                                                                                                                                                                                                                             60 EDDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGP 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---KEDDSYWDPNDEESMNSPCWQVKWOLRQLVRKMILRTSEETISTVOEKQONISPLVR 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116 ERGPORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELV 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 ORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEK 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                176 IHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYK--YTSYPDPILLMKSARNSC--- 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-233 <CL2>
A;Residues: 1-233 <CL2>
A;Cross-references: UNIPROT:Q06599; EMBL:Z14137; NID:g796; PIDN:CAA78511.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Introns: 62/3; 78/1; 94/1
C; Superfamily: tumor necrosis factor
C; Keywords: glycoprotein; lipoprotein; myristylation; transmembrane protein
F; 20/Binding site: myristate (Lys) (covalent) #status predicted
F; 10/Binding site: carbohydrate (Ser) (covalent) #status predicted
F; 145-177/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ------GLLHFGVIGPQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYT----SYPDPILLMKSARNSCWSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----NKPVAHVVA-----DINSPGQLR------WWDSYANALMANGVKLEDNQLV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                   8 GGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           234 DAEYG----LYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEAS-FFG 276
     #status predicted #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 233;
                                                                                                                                                                        89; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 8.8%; Score 130.5; DB 1; Length 1 Similarity 20.3%; Pred. No. 0.0013; 59; Conservative 43; Mismatches 95; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56 IGPQREESPGGP----SINSPLVQT-----LRSSSQASS-
                                                                                                                                                                                                                                                                                                                                                                                                     61 EEQL---PNAFQSIN-PLAQT-----LRSSSRTPS---
                                                                                                                8.9%; Score 131; DB 1;
20.8%; Pred. No. 0.0012;
tive 40; Mismatches 89;
F:19,20/Binding site: myristate (Lys) (covalent)
F:82/Binding site: carbohydrate (Ser) (covalent)
F:146-178/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                        GGPOGSRRCLCLSLFSFLL----VAGATTLF-
                                                                                                                                                                           60; Conservative
                                                                                                                   Query Match
Best Local Similarity
Matches 60; Conserv
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Best Local (
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A;Cross-references: UNIPROT:P29553; GB:M64087; NID:g164244; PIDN:AAA30959.1; PID:g164245
C;Comment: This protein is an important proximal mediator of endotoxemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Introns: 62/3; 79/1; 95/1
C;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; memb
P;78-234/Product: tumor necrosis factor alpha #status predicted <TUM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cross-references: UNIPROT: P33620; EMBL: X62141; NID: 938159; PIDN: CAA44068.1; PID: 938169
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R;Su, X.; Morris, D.D.; McGraw, R.A.
Gene 107, 319-321, 1991
A;Title: Cloning and characterization of gene TNF alpha encoding equine tumor necrosis A;Reference number: JQ1344; MUID:92084125; PMID:1748301
                                                                                                                                                                                                                                                                                                                      DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  182 YYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYT-----SYPDPILLMKSARNSCWSK-- 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 DSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQR 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122 VAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGF 181
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                                                                                                                                                                                                                                                                                                                      Genomic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Superfamily: tumor hecrosis factor
;Keywords: glycoprotein; lipoprotein; myristylation; transmembrane protein
;19,20/Binding site: myristate (Lys) (covalent) #status predicted
;18,18inding site: carbohydrate (Ser) (covalent) #status predicted
;145-177/Disulfide bonds: #status predicted
                                                                                                                                                                           C;Species: Papio sp. (baboon)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Equus caballus (domestic horse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 AMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALPKKTGGPQGSRRCLFLSLFSFLLVAGATTLFCLLHFGVIGPQREEFPK------
                                                                                                                                                                                                                                                                                                                   Sequences of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8.9%; Score 131.5; DB 1; Length 233; 19.2%; Pred. No. 0.0011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---DAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEAS-FFG 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EGAEAKPWYEPIYLGGVFQLEKGDRLSAEINLPDYLDFAESGQVYFG 229
     EGAEAKPWYEPIYLGGVFQLEKDDRLSAEINLPDYLDFAESGQVYFG 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----SLISPLAQA-----VRSSSRTPS----
                                                                                                                                                                                                                                                                                                                from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98;
                                                                                                                                                                                                                          C,Accession: $22052
R,Sanjanwala, M.; Edwarda, A.
submitted to the EMBL Data Library, September 1991
A;Description: Baboon Tumor Necrosis Factor Derived
A;Reference number: $22052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49; Mismatches
                                                                                                                                                tumor necrosis factor alpha precursor - baboon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tumor necrosis factor alpha precursor - horse N; Alternate names: cachectin; TNF alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Introns: 62/3; 78/1; 94/1
                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-233 <SAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
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Best Loca Matches

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C.Genetics:

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A;Status: nucleic acid sequence not shown; translation not shown
A;Status: nucleic acid sequence not shown; translation not shown
A;Status: 1-233 aciRL>
A;Rosiduse: 1-233 aciRL>
A;Cross-references: EMBL:Z15026; NID:G37211; PIDN:CAA78745.1; PID:G37212
A;Cross-references: EMBL:Z15026; NID:G37211; PIDN:CAA78745.1; PID:G37212
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1992
B;Pennica, D.; Nedwin, G.E.; Hayflick, J.S.; Seeburg, P.H.; Derynck, R.; Palladino, M.A.;
Nature 312, 724-729, 1984
A;Title: Human tumour necrosis factor: precursor structure, expression and homology to 1)
A;Reference number: A93351; MUID:85086244; PMID:6392892
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A; Residues: 1-233 <PENN>
A; Cross-treferences: GB:X02910; GB:X02159; NID:g37209; PIDN:CAA26669.1; PID:g37210
A; Orde: this protein was isolated from the monocyte-like cell line HL-60 from a promyeloc
R; Wang, A.M.; Crossey, A.A.; Ladner, M.B.; Lin, L.S.; Strickler, J.; Van Arsdell, J.N.; S
Science 228, 149-154, 1985
A; Title: Molecular cloning of the complementary DNA for human tumor necrosis factor.
A; Reference number: A44189; MUID:85142190; PMID:3856324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N;Alternate names: cachectin; TNPA
C;Species: Homo sapiens (man)
C;Dacession: A93585; Bsequence revision 28-Aug-1985 #text change 09-Jul-2004
C;Accession: A93585; S36153; A93351; A44189; B61478; IS3311; S62610; IS4222; A01646; B23:
R;Nedwin, G.E.; Naylor, S.L.; Sakaguchi, A.Y.; Smith, D.; Jarrett-Nedwin, J.; Pennica, D. Nucleic Acids Res: 13, 6361-6373, 1985
A;Title: Human lymphotoxin and tumor necrosis factor genes: structure, homology and chrom A;Reference number: A93585; MUID:86016093; PMID:2995927
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A;Cross-references: UNIPROT:P01375; GB:X02910; GB:X02159; NID:g37209; PIDN:CAA26669.1; P)
R;Iris, R.J.M.; Bougueleret, L.; Prieur, S.; Caterina, D.; Primas, G.; Perrot, V.; Jurka, Nature enert, 3, 137-145, 1993
A;Title: Dense Alu clustering and a potential new member of the NFkappaB family within a A;Reference number: S36152; MUD:93272029; PMID:8499947
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A;Residues: 1-62, S', 64-233 <WAN>
A;Residues: 1-62, S', 64-233 <WANS
A;Residues: 1, 7, 175-185, 1988
A;Fukuda, S.; Ando, S.; Sanou, O.; Taniai, M.; Fujii, M.; Masaki, N.; Nakamura, K.I.; Anc. Lymphokine Res. 7, 175-185, 1988
A;Futle: Simultaneous production of natural human tumor necrosis factor-alpha, -beta and A;Reference number: A61478; MUID:88301617; PMID:2841543
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A;Residues: 83-102;109-119;121-128,'X',130-131;142-144,'X',146,'XXX',150-152;159-174;180,
A;Residues: 83-102;109-119;121-128,'X',130-131;142-144,'X',146,'XXX',150-152;159-174;180,
A;Marmenout, A.; Fransen, L.; Tavernier, J.; Van Der Heyden, J.; Tizard, R.; Kawashima, I Eur. J. Biochem. 152, 515-522, 1985
Bur. J. Biochem. 152, 515-522, 1985
A;Title: Molecular cloning and expression of human tumor necrosis factor and comparison v A;Reference number: 153311; MUID:86030296; PMID:3932069
                                                                                                                                                                                                                                                                                                                        | | | | | | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | 
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                                                                                                                                                                                                                                  152 NSWESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIY 211
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40 IPSAAQPAHQQL-PTPFTRGTLKPAAHLVGDPSTQDSLRWRANT-----DRAFLR-- 88
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A;Molecule type: DNA
A;Residues: 1-233 <MAR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               194 PSSVFFGAF 202
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Immunogenetics 35, 351-353, 1992
A.Title: Sequence of the tumor necrosis factor/cachectin (TNF) gene from Peromyscus leuc
A.Reference number: I54490; MUID:92218012; PMID:1348497
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C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: 146046; S24641
C;Cludts: 1.; Cleuter. Y.; Kettmann, R.; Burny, A.; Droogmans, L.
Cytokine 5, 336-341, 1993
A;Title: Cloning and characterization of the tandemly arranged bovine lymphotoxin and A;Reference number: 146046; MUID:94083525; PMID:8260599
A;Accession: 146046; MUID:94083525; PMID:8260599
A;Accession: Infoat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tumor necrosis factor alpha precursor - white-footed mouse
C;Species: Peromyscus leucopus (white-footed mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C;Accession: IS4490
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                                                                                             ---WSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEAS-FFG 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 35;
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Superfamily: tumor necrosis factor
Keywords: glycoprotein; hipoprotein; myristylation
19,20/Binding site: myristate (Lys) (covalent) #status predicted
84/Binding site: carbohydrate (Ser) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2; Length 235;
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ilarity 24.9%; Pred. No. 0.002;
Conservative 29; Mismatches 78;
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8.8%; Score 129.5; DB 2; 24.5%; Pred. No. 0.0016; tive 39; Mismatches 75;

Local Similarity 24.59 les 45; Conservative

Best Loc Matches

셤 8 셤 ઠ 셤 ઠે 셤

Query Match

lymphotoxin - bovine

RESULT 14

324641

C;Genetics: A,Introns: 32/3; 68/1 C;Superfamily: tumor necrosis factor

A; Residues: 1-204 < CL2> A; Cross-references: UNI

Query Match Best Local Similarity

47;

Best Loca Matches

8,

A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA

A; Residues: 1-235 < RES>

A; Gene: PlTNF

Genetics

A; Accession: 154490

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() D'Alfonso, S.; Richiardi, P.M.

Immunogenetics 39, 150-154, 1994

I,Title: A polymorphic variation in a putative regulation box of the TNFA promoter regic

I,Faference number: 154522; MUID:94102809; PMID:7903959

I,Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:S68530; NID:g544751

R;Stevenson, F.T.; Bursten, S.L.; Locksley, R.M.; Lovett, D.H.
J. Exp. Ward 176, 1053-1062, 1992

A;Title: Myristyl acylation of the tumor necrosis factor alpha precursor on specific lystaference number: A59163; MUID:93018820; PMID:1402651

A;Reference number: A59163; MUID:93018820; PMID:1402651

A;Reference number: A59163; MUID:93018820; PMID:1402651

B;Aggarwal, B.B.; Kohr, W.J.; Hass, P.E.; Moffat, B.; Spencer, S.A.; Henzel, W.J.; Bring J. Biol. Chem. 260, 2345-2354, 1985

J. Biol. Chem. 260, 2345-2354, 1985

A;Title: Human tumor necrosis factor. Production, purification, and characterization.
A;Reference number: A92511; MUID:85130974; PMID:3871770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Superfamily: tumor necrosis factor
C; Keywords: cytokine; cytotoxin; glycoprotein; homotrimer; lipoprotein; lymphokine; macz
C; Keywords: cytokine; cytotoxin; glycoprotein; homotrimer; lipoprotein; lymphokine; macz
F; 17-233/Product: tumor necrosis factor #status experimental <MAT>
F; 19, 20/Binding site: myristate (Lys) (covalent) #status experimental
F; 81/Binding site: carbohydrate (Ser) (covalent) (partial) #status experimental
F; 145-177/Disulfide bonds: #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Comment: Secreted from mitogen-activated macrophages within 4-24 hours after induction out detriment to normal cells. It can also act synergistically with interferon gamma to C;Comment: TNF-alpha and -beta (lymphotoxin) are the products of different genes closely ut are produced by different cell types and have different induction kinetics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQR 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122 VAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGF 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65
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                                                   R;Takakura-Yamamoto, R.; Yamamoto, S.; Fukuda, S.; Kurimoto, M.
Eur. J. Blochem. 235, 431-437, 1996
A;Title: O-Glycosylated species of natural human tumor-necrosis factor-alpha.
A;Reference number: $62610; MUID:96202967; PMID:8631363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 AMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16 ALPKKTGGPQGSRRCLFLSLFSFLIVAGATTLFCLLHFGVIGPQREEFPR-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.5%; Score 125.5; DB 1; Length 233;
17.8%; Pred. No. 0.0036;
rative 52; Mismatches 99; Indels 85; Gaps
Cross-references: GB:M26331; NID:g339763; PIDN:AAA36758.1; PID:g339764; Experimental source: U-937 cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---DAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEAS-FFG 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GDB:120441; OMIM:191160
A;Map position: 6921.3-6921.3
A;Introns: 62/3; 78/1; 94/1
C;Complex: homotrimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 17.8*
Matches 51; Conservative
                                                                                                                                                                                                                                            A; Molecule type: protein A; Residues: 77-99 <TAK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Residues: 1-8 <DAL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Gene: GDB: TNF; TNFA
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Search completed: June 3, 2005, 06:25:41 Job time : 42 secs This Page Blank (uspto)

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GenCore version 5.1.6
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OM protein - protein search, using sw model Run on:

3, 2005, 06:07:44 ; Search time 176 Seconds (without alignments) 817.581 Million cell updates/sec June

US-10-662-431-2 1478 1 MAMMEVQGGPSLGQTCVLIV.....NEHLIDMDHEASFFGAFLVG 281 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 Total number of hits satisfying chosen parameters:

1612378 seqs, 512079187 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

	Description	P50591 homo sapien	Q8k3g0 rattus norv	P50592 mus musculu	Q7t1f2 qallus qall					Q6jsd9 homo sapien		035235 m tumor nec		P41047 mus musculu		P48023 homo sapien	_	P63307 macaca mula	P63306 macaca neme		Q9i8d8 gallus gall	Q9bea8 sus scrofa	Q8k3y8 mus musculu	Q861w5 felis silve	P36940 rattus norv	Q9wv90 marmota mon	Q80yz0 mus musculu	Q8k3y7 rattus norv	Q8nfe9 homo sapien		Q6j3q6 canis famil	095150 homo sapien
SUMMARIES	ID	TN10 HUMAN	Q8K3 <u>G</u> 0	TN10 MOUSE	Q7T1F2	Ферндэ	Q7ZYX9	O90WT9	Q9DDZ5	Q6JSD9	TN11 RAT	TN11 MOUSE	TN11 HUMAN	TNF6_MOUSE	TNF6_CERTO	TNF6_HUMAN	TNF6_MACFA	TNF6 MACMU	TNF6_MACNE	Q7TMV9	TNFS_CHICK	TNF6_PIG	Q8K3Y8	Q861W5	TNF6 RAT	09WV90	Q80YZ0	Q8K3Y7	Q8NFE9	TNF5_BOVIN	Q6J3Q6	TN15_HUMAN
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d	Query Match	100.0	65.2	62.9	54.8	39.1	22.6	20.8	20.7	19.7	18.1	17.5	17.0	12.8	12.7	12.6	12.5	12.5	12.5	12.5	12.4	12.3	12.2	12.1	12.0	11.9	11.8	11.7	11.2	11.1	11.1	10.8
	Score	1478	963	930	809.5	577.5	334.5	307.5	305.5	291	267.5	258.5	251.5	189.5	187	186	185	185	185	184.5	184	182	180	178.5	177.5	175.5	175	173	166	164	٠	160
	Result No.	н	7	m	4	ß	9	7	8	σ.	10	11	12	13	14	15	16	17	18	19	20	2.1	22	23	24	25	56	27	28	53	30	31

043557 homo sapien Q8mj19 macaca mula	Q7t2q3 cyprinus ca Q9qyh9 mus musculu Q9bdn3 callithrix	QSbCms accus tivi 097605 felis silve Q6u817 lateolabrax D63305 carcocabus	P63304 macaca mula 097626 canis famil P29965 homo sapien	070332 mesocricetu Q95mq5 sus scrofa
TN14 HUMAN Q8MJ19	Q7T2Q3 TN14_MOUSE TNF5_CALJA	INFS ACTIK TNFS FELCA Q6U817 TNFS CEPTO	TNFS_MACMU TNFS_CANFA TNFS_HUMAN	0703 <u>3</u> 2 TNF5_PIG
4 2	244			7 7
240	227	260 241 241	261 260 261	216 261
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159.5	153.5	149.5 149	148 147.5 147.5	144.5
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ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0005887; C:integral to plasma membrane; TAS.
GO; GO:0005225; C:soluble fraction; TAS.
GO; GO:0005102; F:receptor binding; TAS.
GO; GO:0007267; P:coll-cell sinding; TAS.
GO; GO:0007267; P:coll-cell sinding; TAS.
GO; GO:0007123; P:positive regulation of I-kappaB kinase/NF-k. .; IEP.
GO; GO:0007165; P:signal transduction; TAS.
InterPro; IPR006052; TWF family.
InterPro; IPR008983; TWF family.
                                                                                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 114-281.

MEDLINE=99413670; PubMed=10485660; DOI=10.1016/S1074-7613(00)80100-4; Cha S.-S., Kim M.S., Choi Y.H., Sung B.J., Shin N.K., Shin H.C., Sung Y.C., Oh B.-H.;

"2.8 A resolution crystal structure of human TRAIL, a cytokine with selective antitumor activity.";

"1.8 A resolution crystal structure of numan TRAIL, a cytokine with selective antitumor activity.";

"Immunity 11:253-261(1999).

"PRESF10B/TRAILR2, TNFRSF10C/TRAILR3, TNFRSF10A/TRAILR1,

"PRESF10B/TRAILR2, TNFRSF11B/OPG. Induces apoptosis. Its activity may be modulated by binding to the decoy receptors

TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and TNFRSF11B/OPG that cannot
                                                        MEDLINE=20017054; PubMed=10549288; DOI=10.1016/S1097-2765(00)80207-5; Hymowitz S.G., Christinger H.W., Fuh G., Ultsch M., O'Connell M., Kelley R.F., Ashkennazi A., de Vos A.M.;
"Triggering cell death: the crystal structure of ApozL/TRAIL in a complex with death receptor 5.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SUBUNIT: Homotrimer.
-!- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
-!- TISSUB SPECIFICITY: Widespread; most predominant in spleen, lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      induce apoptosis. COFACTOR: Binds 1 zinc ion and one anionic solvent molecule per
                                                                                                                                                                                 PubMed=10542098; DOI=10.1038/14935; Mongkolsapaya J., Grimes J.M., Chen N., Xu X.-N., Stuart D.I., Jones E.Y., Screaton G.R.; "Structure of the TRAIL-DR5 complex reveals mechanisms conferring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: Belongs to the tumor necrosis factor family.
                Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                             X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 114-281.
                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 119-281.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U37518; AAC50332.1; --
EMBL; U57059; AAB01233.1; --
EMBL; BC032722; AAH32722.1; --
PDB; 1D0G; X-ray; A/B/D-114-281.
PDB; 1D2Q; X-ray; A=114-281.
PDB; 1D4V; X-ray; B=119-281.
PDB; 1DG6; X-ray; B=119-281.
PDB; 1DG7; X-ray; D/E/F/J/K/L=114-281.
Genew; HGNC:11925; TNFSF10.
MIM; 603598; --
MIM; 603598; --
                                                                                                                                                                                                                                                  specificity in apoptotic initiation.";
Nat. Struct. Biol. 6:1048-1053(1999).
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SMART; SM00207; TNF; 1.
 mouse cDNA sequences.";
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PROSITE; PS00251; TNF_1; 1.
                                                                                                                                      Mol. Cell 4:563-571(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and prostate.
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FYYIKSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MAMMEVOGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          narlus Joyagusa (mar).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
         3D-structure; Apoptosīs; Cytokine; Metal-binding; Signal-anchor;
Transmembrane; Zinc.
                                                        Signal-anchor for type II membrane protein (Potential). Extracellular (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                         ,
0
                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 1478; DB 1; Length 281; 100.0%; Pred. No. 4.4e-113; ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
                                                                                                                                                                                                                                                                                                                                                                                  32509 MW; DDAAAF78DAAB2F6D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
                                            Cytoplasmic (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TNF-related apoptosis inducing ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last seq
01-MAR-2004 (TrEMBLrel. 26, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STREALN=DA,
STREALN=DA,
STREALS A.M. Giegerich G.;
Submitted (MAY-2002) to the EMBL/G
EMBL, AVILS578; AAM49797.1; -.
HSSP; P50591; 1D2Q.
GO: GO:0016020; C:membrane; IEA.
PROSITE; PS50049; TNF_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 281; Conservative
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                                                                                     Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                  281 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                      181
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                                                           PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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Q8K3G0;
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                                          DOMAIN
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62.9%; Score 930;
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01-OCT-2003 (TrEMBLrel. 25, Created)
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52 52 N
291 AA; 33477 MW;
                                                                                                                                                                                                                                                                                      65.68;
                                                                                                                                                                                                                                                                                                Matches 177; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                 17
                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rissum=Spleen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=TRAIL;
                                                                                                                                                                                                           TRANSMEM
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Best Local (
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                                                                                                                                                                                                                                                        SEQUENCE
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Q7T1F2
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                                                                                                                                                                                                                                                                                        188
                                                                                                                                                                                                                                                                                                                         65 WDPNDEESMNSPCWQVKWQLRQLVRKMILRTSERTISTVQEKQQNISPLVRERGPQRVAA 124
                                                                                                                                                                                                                                  185 YSQTYFRFQE--EIKENTKND----KQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYG 238
                                                                                                                                                                                                                                                                  HITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFYYI 184
                                                                                                                                                                                                68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 GPSLGQ----TCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKEDDSY
                                                                                                                                                                                       SEQUENCE FROM N.A. MRDIALINE-96111955; PubMed=8777713; DOI=10.1016/1074-7613(95)90057-8; Wiley S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P., Nicholl J.K., Sutherland G.R., Davis-Smith T., Rauch C., Smith C.A., Goodwin R.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-077-1996 (Rel. 34, Created)
01-077-1996 (Rel. 34, Last sequence update)
01-077-1996 (Rel. 34, Last sequence update)
05-17LJ-2004 (Rel. 44, Last annotation update)
Tumor necrosis factor ligand superfamily member 10 (TNF-related apoptosis inducting ligand) (TRAIL protein).
Name-Infeflo; Synonyms-Trail;
Mus musculus (Mouse)
                                                                                                                                                       10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --- SUBUNIT: Homotrimer (By similarity).
--- SUBUNIT: Homotrimer (Potential)
--- SUBCELLULAR LOCATION: Type II membrane protein (Potential)
--- IISSUB SPECIFICITY: Widespread.
--- SIMILARITY: Belongs to the tumor necrosis factor family.
  factor receptor binding; IEA
                                                                                                                               Query Match 65.2%; Score 963; DB 2; Length 287; Best Local Similarity 67.7%; Pred. No. 8.5e-71; Matches 189; Conservative 29; Mismatches 51; Indels
                                                                                   PROSITE; PS00251; TNF 1; UNKNOWN 1.
PROSITE; PS50049; TNF 2; 1.
SEQUENCE 287 AA; 32979 MW; CA4F5B5D7C833FEC CRC64;
                                                                                                                                                                                                                                                                                                                                                        277
                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                         LYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGA
                                                                                                                                                                                                                                                                                                                                                                                                                                  291 AA
GO; GO:0005164; F:tumor necrosis factor r
GO; GO:0006955; P:immune response; IEA.
InterPro; IPR006052; TNF_IME.
InterPro; IPR008983; TNF_IME.
InterPro; IPR003636; TNF_Subf.
ProDom; PD00229; TNF; 1.
SMART; SM00207; TNF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            201 DASKOVSKDKVRTKQLVQYIYKYTSYPDPIVLMKSARNSCWSRDAEYGLYSIYQGGLFEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 ICIVLLQVLLQAVSVAVTYMYFTNEMKQLQDNYSKIGLACFSKTDEDFWDSTDGEILNRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        137 SSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----IKENTKONDKONOYIYKYTSYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 VLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKEDDSYWDPNDEESMNSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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"Molecular Cloning and Characterization of Chicken Tumor Necrosis
Factor (TMF)-Superfamily Ligands, CD30L and TNF-Related Apoptosis
Inducing Ligand (TRAIL).",
J. Vet. Med. Sci. 66:643-650(2004).
EMBL; AB114678; BAC79267.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Signal-anchor for type II membrane protein (Potential).

Extracellular (Potential).

N-linked (GloNAc. . ) (Potential).

3FEACAB9F0D7D802 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50; Indels
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01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Tumor necrosis factor related apoptosis inducing ligand.
                                                                                                                                                                              EMBL, U37522; AAC52345.1; -.
HSSP, P50531; 1D2Q.
MGD; MGI:107414; Thfsf10.
InterPro; IPR006052; TNF family.
InterPro; IPR008983; TNF_like.
InterPro; IPR003636; TNF_subf.
ProDom; PD002029; TNF; 1.
ProDom; P000229; TNF; 1.
ProDom; TNF 1.
PROSITE; P800251; TNF; 1.
PROSITE; P850049; TNF 2; 1.
PROSITE; P850049; TNF 2; 1.
Apoptosis; Cytokine; Signal-anchor; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cytoplasmic (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Pred. No. 4.4e-68; 37; Mismatches 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               251 KENDRIFVSVTNEHLIDMDHEASFFGAFLV 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                261 KKNDRIFVSVTNEHLMDLDQEASFFGAFLI 290
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Similarity
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Name=tnfsf101;
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Matches
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MEDINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

MA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Diatchenko L., Marnsina K., Farmer A.A., Rubin G.M., Hong L.,

Bromstein M.J., Usdin T.B., Toshlywis S., Carninci P., Schaefer C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Pahey J., Helton E., Retteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rizywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68 N----DEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQ-EKQQNISPLVRERGPQ- 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 ---RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIH 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  178 EKGFYYIYSQTYFRFQEE-----IKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCW 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123 PILKIAAHLTGSSKRSSA-SPHNYLSYRGIGHKIHSWESSRRGHSFLYNVELWNGELVVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 GGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKEDDSYWDP
                                                                                                                                                                                                                                                                                                                                                                                                                                          19; Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV 280
                    GG; GO:0016020; C:membrane; IEA.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
GO; GO:0006955; F:tumor response; IEA.
InterPro; IPR006052; TNF family.
InterPro; IPR008983; TNF like.
InterPro; IPR008983; TNF like.
InterPro; IPR008029; TNF like.
Prom; P000229; TNF in subf.
Prom; P000229; TNF in subf; 1.
PROSITE; PS00251; TNF i.
PROSITE; PS50049; TNF 2; 1.
SEQUENCE 304 AA; 34658 MW; DFC128B517747C96 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54.8%; Score 809.5; DB 2; Length 304; 55.4%; Pred. No. 3.6e-58; ive 45; Mismatches 65; Indels 19
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 55.4%
Matches 160; Conservative
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HSSP; P50591; 1D2Q.
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NCBI_TaxID=7955;
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75 SPCWQVKWQLRQLVRK-MILRTSEETISTVQEKQQNISPLV----RERGPQRVAAHITG 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YFR---FQEEIKENTKND------KQMVQYIY-KYTSYPDPILLMKSARNSCWSK 233
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'Generation and initial analysis of more than 15,000 full-length human
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STRAIN=AB; TISSUE=Whole body;
STRAIN=AB; TISSUE=Whole body;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausnar R.D., Collins F.S., Wagnar L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max. S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
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Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes,
Cyprinidae, Danio.
                                                                                                                                                                                                                           TISSUE=Whole;
Strausberg R.;
Strausberg R.;
Strausberg R.;
Strausberg R.;
Submitted (JUL_2004) to the EMBL/GenBank/DDBJ databases.
EMBL, BCO76005; AAM76005.1; -.
GO; GO:0001604; F:tumor necrosis factor receptor binding; IEA.
GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
GO; GO:0006955; P:immune response; IEA.
R InterPro; IPR008983; TWF famlly.
R InterPro; IPR008983; TWF like.
R InterPro; IPR008983; TWF like.
R PF00209; TWF; 1.
R PRODOM; PD002012; TWF; 1.
R PROSITE; PS002012; TWF 1; 1.
R PROSITE; PS00049; TWF 2; 1.
SEQUENCE 299 AA; 33526 MW; BA776793D2F11ED5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Length 299;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      252 DSEYGLYSIYQAGLFQLGSGDRVFVTVSNVSTIDMDEKSSFFGAFLV 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82; Indels
                                                                                 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39.1%; Score 577.5; DB 2
42.2%; Pred. No. 3.9e-39;
cive 57; Mismatches 82
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                                                        sednences.
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Fri Jun

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Bridgham J.T., Johnson A.L.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases
EMBL; AYOS7941, AAL23702.1; --
HSSP; P50591; 1D2Q.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                          SEQUENCE
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         SORRERE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LFGEPCMKLAEGIKAYISKVTDSIISKQTLHAARTRTHSYNTTGSKFMTTV-----MQ 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 RVAAHITGTRGRSNT----LSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELV 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             176 IHEKGFYYIYSQTYFRF-QEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKD 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18 LIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACF----LKEDDSYWDPND-EE
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
TNF-related apoptosis inducing ligand-like protein.
Gallus gallus (Chicken).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33;
                                                                                                                                                                                                                                                                                                                                                                           Strausberg, R.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, BC044336, AA444336.1; -.
HSSP; BC044336, AA444336.1; -.
EMBL, EDC04336, AA444336.1; -.
ZIN, ZDB-GENB-010801-1; tnfsf101.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0005164, F:tumor necrosis factor receptor binding; IEA.
GO; GO:000555; P:immune response; IEA.
InterPro; IPR006055; TNF family.
InterPro; IPR008093; TNF like.
InterPro; IPR008036; TNF Bubf.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22.6%; Score 334.5; DB 2; Length 317; 29.2%; Pred. No. 3.7e-19; tive 55; Mismatches 113; Indels 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50049; TNF 2; 1.
317 AA; 35465 MW; 68F76BC1A40DCE9F CRC64;
                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF0022; TNF; 1.
ProDom; PD002012; TNF subf; 1.
SMART; SM00207; TNF; 1.
PROSITE; PSS0049; TNF_2; 1.
                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=AB; TISSUE=Whole body;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 29.29
108 83; Conservative
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Matches
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67 PNDEESM-NSPCWQVKWQLRQLVRKMILRTSEETI--STVQEKQO---NISP-LVRERGP 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 QRVAAHI-----TGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLR 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          171 NGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDFILLMKSARNSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18 LIVIFTVLLQ--SLCVAVTYVYFT-----NELKQM--QDKYSKSGIACFLKEDDSYWD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124 GKPSAHLIFRPQNPAQDGSSRRFGNLS-----QSCRHAITRWEDS-TIHSHLQNITYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 LIHAFSLELQLIPLCTAPEWAEGTWSQALQGNAFPRLKAQSQGSSEELRCLQLINQQQEG
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bobe J., Goetz F.W.;
"Molecular cloning and expression of a TNF receptor and two TNF ligands in the fish overy.";
Comp. Biochem. Physiol. B, Comp. Biochem. 129:475-481(2001).
EMBL, AR250041; AR347640.1;
-...
ZFIN; ZDB-GENE-010801-1; tnfef101.
                                                                                                                                                                                                                                                                                                                                                                  39;
GO; GO:0016020; C:membrane; IEA.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
GO; GO:000695; F:tumor response; IEA.
PRINTS; PR01234; TNECROSISFCT.
PRODERT; SM02021; TNF subf; 1.
PROSITE; PS50049; TNF_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0016020; C:membrane; IEA.
GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
                                                                                                                                                                                                                                                                                                        20.8%; Score 307.5; DB 2; Length 287; 32.3%; Pred. No. 5.3e-17; Live 46; Mismatches 110; Indels 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            231 WSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              550049; TNF 2; 1.
287 AA; 32092 MW; DB06E1C95087B108 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   214 AA; 24093 MW; 98C002474FF691AA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brachydanio rerio (Zebrafish) (Danio rerio).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO; GO:0006955; P:1mmune response; IEA.
InterPro; IPR006052; TNF family.
InterPro; IPR008983; TNF like.
InterPro; IPR003636; TNF subf.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00229; TNF; 1.
ProDom; PD002012; TNF subf; 1.
SMART; SM00207; TNF; 1.
PROSITE; PS50049; TNF 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2001 (TrEMBLrel. 16, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                        Query Match 20.8
Best Local Similarity 32.3
Matches 93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRAIL-like protein.
Name=tnfsf101;
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Transmembrane.
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONFLICT
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                                                                  47 QRPSAHLTLSSASDNSRPQSDMHQPQFDLHQSCRHPVHTW-ANKSFGAHLYNMTLTNGRL 105
                                                                                                            120 QRVAAHITGTRGRSNT----LSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGEL 174
                                                                                                 175 VIHEKGFYYIYSQTYFRF-QEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSK 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09ESE2; 091219;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Tumor necrosis factor ligand superfamily member 11 (Receptor activator of nuclear factor Rappa B ligand) (RANKL) (TMF-related activation-induced cytokine) (TRANCE) (Osteoprotegerin ligand) (Obtooclast differentiation factor) (ODF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=20540945; PubMed=11092398;
Xu J.K., Tan J.K., Huang L., Gao X.H., Laird R., Liu D., Wysocki S.,
                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Lung carcinoma;
Polvi A., Ruosaari S., Vendelin J., West A., Saarikko I.,
Reinikainen A., Hollmen J., Laitinen T., Mannila H., Lahesmaa R.,
                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39 TNELKOMODKYSKSGIACFLKEDDSYWDPNDEESMNSPCWQVKWQLRQLVRK 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TNELKQMQDKYSKSGIACFLKEDDSYWDPNDEESMNSPCWQVKWQLRQLVRK 52
                             1,
         Length 214;
                                                                                                                                                        234 DAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
                                                                                                                                                                                                                                                                               member
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19.7%; Score 291; DB 2; Length 63; 100.0%; Pred. No. 1.7e-16;
                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  Kere J.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY312579; AAR16184.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             63 AA; 7638 MW; 8F0C7936DA5AA6E6 CRC64;
                                                                                                                                                                                                                                             05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Chemokine tumor necrosis factor ligand superfamily n
         20.7%; Score 305.5; DB 2; 37.6%; Pred. No. 5.3e-17; ive 37; Mismatches 59;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            318 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=Tnfsf11; Synonyms=Opgl, Rankl, Trance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.08;
                   Local Similarity 37.6%
Les 62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
TISSUE=Tibial bone;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                          (Fragment).
Name=TNFSF10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
           Query Match
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                                                                                                                                                                                                                         Q6JSD9
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                               Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11;
                                                                                                                                                                                                                                                                                                     Marks S.C. Jr.,

"Evidence that the rat osteopetrotic mutation toothless (tl) is not in

"Evidence that the rat osteopetrotic mutation toothless (tl) is not in

"Evidence that the rat osteopetrotic mutation and activation factor.

"In It. J. Dev. Biol. 45:853-859(2001).

"In TURNSFILA/RANK. Osteoclast differentiation and activation factor.

"TURNSFILA/RANK. Osteoclast differentiation and activation factor.

Augments the ability of dendritic cells to stimulate naive T-cell

proliferation. May be an important regulator of interactions

between T cells and dendritic cells and may play a role in the

regulation of the T cell-dependent immune response. May also play

an important role in enhanced bone-resorption in humoral

hypercalcemia of malignancy.

"Is SUBCELIULAR LOCATION: Type II membrane protein and secreted (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43 PAASREMFLALLGLGLGQVVCSIALFLYFRAQMD--PNRISEDSTRCFYRILRLRENTGL 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 PSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACF----LKED--- 61
                                                                                                                                                                                                                                                                                                                                                    ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tumor necrosis factor ligand superfamily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tumor necrosis factor ligand superfamily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE SPECIFICITY: Highly expressed in thymus and bone tissues.
                                                                                                                                                                          STRAIN=Fischer 344;
BEDLINES-1562371, PubMed=11804028;
Odgren P.R., Kim N., van Wesenbeeck L., MacKay C., Mason-Savas A., Safadi F.F., Popoff S.N., Lengner C., van-Hul W., Choi Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cytokine; Differentiation; Glycoprotein; Receptor; Signal-anchor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Organia americal).

Extracellular (Potential).
Cleavage (By similarity).
N-linked (GlcNAc. . ) (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cytoplasmic (Potential).
Signal-anchor for type II membrane
"Cloning, sequence and functional characterization of the rat homologue of receptor activator of NF-kB ligand."; J. Bone Miner. Res. 15:2178-2186 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18.1%; Score 267.5; DB 1; Length 318; 27.3%; Pred. No. 1.2e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            proteolytic processing (By similarity). SIMILARITY: Belongs to the tumor necrosis factor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- PTM: The soluble form derives from the membrane form by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55; Mismatches 106; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35370 MW; 4B87A4D706AD098F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            member 11, membrane form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 member 11, soluble form.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 I -> M (in Ref.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF422001.
HSSP; 035235; 1072.
RGD; 620784; Thfefil.
InterPro; IPR006652; TNF family.
InterPro; IPR008983; TNF like.
InterPro; IPR008983; TNF like.
InterPro; IPR008983; TNF subf.
Pfam; PF00229; TNF; 1.
ProDom; PD002012; TNF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF187319; AAG17031.1; -. EMBL; AF425669; AAL23963.1; -.
                                                                                                                                         SEQUENCE OF 266-318 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               318
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68
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140
199
264
317
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Fri

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QDSTLESEDTEALPDSCRRMKQAFQ------GAVQRELQHIV-----GPQ 139
                                                                                                                                                             162 SFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYT-SYPDPI 220
                                                                                                                                                                                                                                                                     - DSYWDPNDEESMINSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
                                                                                 R---VAAHITGT-----RGRS------NTLSSPNSKNEKALGRKINSWESSRSGH 161
                                                                                                                                                                                     221 LLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV 280
                                                                                                                      140 RFSGVPAMMEGSWLDVARRGKPEAQPFAHLTINAADIPSGSHKVSL----SSWYHDR-GW 194
                                                                                                                                                                                                                                                                                                                                                                                       TMIL MOUSE STANDARD; PRT; 316 AA.

03525; 035306; Q9JJK8; Q9JK9; Q9R1Y0;
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2004 (Rel. 45, Last annotation update)
25-OCT-2004 (Rel. 45, Last annotation update)
Tumor necrosis factor ligand superfamily member 11 (Receptor activator of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-induced cytokine) (TRANCE) (Gsteoptoregerin ligand) (OPGL) (Osteoclast differentiation factor) (ODF) (Osteoclastogenesis-inhibitory factor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Choi Y.;
"TRANCE is a novel ligand of the tumor necrosis factor receptor family that activates c-Jun N-terminal kinase in T cells.";
J. Biol. Chem. 272:25190-25194 (1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   homologue of the TNF receptor and its ligand enhance T-cell growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          四
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=97460112; PubMed=9312132; DOI=10.1074/jbc.272.40.25190; Wong B.R., Rho J., Arron J., Robinson E., Orlinick J., Chao M., Kalachikov S., Cayani E., Bartlett F.S. III, Frankel W.N., Lee S.Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Bone marrow;
MEDLINE=98227661; PubMed=9568710; DOI=10.1016/S0092-8674(00)81569-X;
Lacey D.L., Timms E., Tan H.-L., Kelley M.J., Dunstan C.R.,
Burgess T., Elliott R., Colombero A., Elliott G., Scully S., Hsu H.,
Sullivan J., Hawkins N., Davy E., Capparelli C., Eli A., Qian Y.-X.,
Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Bone marrow stroma;
MEDLINE=98188248; PubMed=9520411; DOI=10.1073/pnas.95.7.3597;
Yasuda H., Shima N., Nakagawa N., Yamaguchi K., Kinosaki M.,
Mochizuki S.-I., Tomoyasu A., Yano K., Goto M., Murakami A., Tsuda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cytokine that regulates osteoclast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUB=Thymic lymphoma;
MEDLINE=98032977; Pubmed=9367155; DOI=10.1038/36593;
Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.
Tometsko M.E., Roux B.R., Teepe M.C., Dubose R.F., Cosman D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=Tnfsf11; Synonyms=OPGL, RANKL, Trance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Osteoprotegerin ligand is a cytol differentiation and activation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM 1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and dendritic-cell function.";
Nature 390:175-179(1997).
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Cell 93:165-176(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Hybridoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
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MEDLINE-21839021; PubMed-11733492; DOI-10.1074/jbc.M106525200;
Ito S., Wakabayashi K., Ubukata O., Hayashi S., Okada F., Hata T.;
"Crystal structure of the extracellular domain of mouse RANK ligand at
Morinaga T., Higashio K., Udagawa N., Takahashi N., Suda T.; "Osteoclast differentiation factor is a ligand for osteoprotegerin/osteoclastogenesis-inhibitory factor and is identical
                                                                                                                                                                                                                                                                                                                                                                                                                      nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.2-A resolution...
J. Biol. Chem. 277:6631-6636 (2002).
-!- FUNCTION: Cyrokine that binds to TNFRSFIIB/OPG and to
TNFRSFIIA/RANK. Osteoclast differentiation and activation factor.
Augments the ability of dendritic cells to stimulate naive T-cell proliferation. May be an important regulator of interactions between T cells and dendritic cells and may play a role in the regulation of the T cell-dependent immune response. May also play an important role in enhanced bone-resorption in humoral hypercalcemia of malignancy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isoid=035235-3; Sequence=VSP_006448; TISSUE SPECIFICITY: Highly expressed in thymus and lymph nodes, but not in nonlymphoid tissues and is abundantly expressed in T cells but not in B cells. A high level expression is also seen in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PTM: The soluble form of isoform 1 derives from the membrane form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      by proteolytic processing. The cleavage may be catalyzed by ADAM17. A further shorter soluble form was observed.
-!- DISEASE: Deficiency in Infsfil results in failure to form lobulo-
                                                                                                                                                                                      MEDLINE=99214075; PubMed=10196481; DOI=10.1016/S0378-1119(99)00025-6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=99240759; PubMed=10224132; DOI=10.1074/jbc.274.19.13613; Lum L., Wong B. R., Josien R., Becherer J.D., Erdjument-Bromage H., Schloendorff J., Tempst P., Choi Y., Blobel C.P.; Erdjument a role of a tumor necrosis factor-alpha (TNF-alpha)-converting enzyme-like procease in shedding of TRANCE, a TNF family member involved in osteolastogenesis and dendritic cell survival.". J. Biol. Chem. 274:13613-13618(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIINE=21464816; PubMed=11581298; Lam J., Nelson C.A., Ross F.P., Teitelbaum S.L., Fremont D.H.; "Crystal structure of the TRANCE/RANKL cytokine reveals determinants of receptor-ligand specificity.";
                                                                                                                                                                                                              Kodaira K., Kodaira K., Mizuno A., Yasuda H., Shima N., Murakami A.,
                                                                                                                                                                                                                               Ueda M., Higashio K.; "Cloning and characterization of the gene encoding mouse osteoclast differentiation factor.";
                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21150053; PubMed=11250921; DOI=10.1210/en.142.4.1419;
Reda T., Kasai M., Utenyama M., Hirokawa K.;
"Determination of three isoforms of the receptor activator of nucle
factor-kappaB ligand and their differential expression in bone and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SÜBUNIT: Homotrimer.

SUBCELLULAR LOCATION: Type II membrane protein and secreted (isoforms 1 and 2); Cytoplasmic (isoform 3).

ALTERNATUE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 139-147, PROCESSING, AND N-GLYCOSYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bvent=Alternative splicing; Named isoforms=3;
                                                                                    Proc. Natl. Acad. Sci. U.S.A. 95:3597-3602(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 158-316.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 137-316.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IsoId=035235-2; Sequence=VSP_006449;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IsoId=035235-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clin. Invest. 108:971-979(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Endocrinology 142:1419-1426(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the trabecular bone and lung. PTM: N-glycosylated.
                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM 1).
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alveolar mammary structures during pregnancy, resulting in death of newborns. Trance-deficient mice show severe osteopetrosis, with no osteoclasts, marrow spaces, or tooth enuption, and exhibit profound growth retardation at several skeletal sites, including the limbs, skull, and vertebrae and have marked chondrodysplasia, with thick, irregular growth plates and a relative increase in hypertrophic chondrocytes.
SIMILARITY: Belongs to the tumor necrosis factor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSEEMGSGPGVPHEGPLHPAPSAPAPAPPPA -> TP (in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  member 11, membrane form.
Tumor necrosis factor ligand superfamily
member 11, soluble form.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tumor necrosis factor ligand superfamily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct protein sequencing; Glycoprotein; Receptor; Signal-anchor; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:005515; F: procein binding; IPI.
GO; GO:0042804; F: procein homooligomerization activity; IDA.
GO; GO:004545; P: bone resorption; IDA.
GO; GO:0004587; P: organogenesis; IMP.
GO; GO:0001503; P: osgification; IMP.
GO; GO:000503; P: regulation of osteoclast differentiation; IDA.
InterPro; IPR008083; TNF [amily.
InterPro; IPR008983; TNF [amily.
InterPro; IPR008635; TNF_labe.
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N-linked (GLONAC. . .) (Potential).
N-linked (GLONAC. . .) (Potential).
Missing (in isoform 3).
FTId=VSP 006448.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Signal-anchor for type II membrane protein (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3D-structure; Alternative splicing; Cytokine; Differentiation;
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G -> D (in Ref. 2).

Missing (in Ref. 5)
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                                                                                                                                                                                                                                                                                            EMBL, AF053713, AAC40113.1; EMBL, AB008426; BAA25425.1; EMBL, AB02039; BAA36970.1; CMBL, AB022036; BAA36970.1; GMBL, AB022037; BAA36970.1; JOINED. EMBL, AB022037; BAA36970.1; JOINED. EMBL, AB032771; BAA37257.1; EMBL, AB032772; BAA37259.1; CMBL, AB032772; BAA37259.1; CMBL, AB036778; BAA37259.1; CMBL, AB036778; BAA37259.1; CMBL, AB03678; AF467316.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE, PS00251; TNF 1; FALSE_NEG.
PROSITE; PS50049; TNF_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00229; TNF; 1.
ProDom; PD002012; TNF subf; 1.
SMART; SM00207; TNF; 1.
                                                                                                                                                                                                                                                                    EMBL; AF013170; AAC71061.1; -. EMBL; AF019048; AAB86812.1; -.
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VARSPLIC
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-----VRERGPQRVA--AHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLS 165
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014788; 014723; 096017; 09P203;
116-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2004 (Rel. 44, Last annotation update)
05-UUL-2004 (Rel. 44, Last annotation update)
05-UUL-2004 (Rel. 44, Last annotation update)
indo necrosis factor ligand superfamily member 11 (Receptor activator of nuclear factor kappa B ligand) (RANKL) (TNF-related activationiduced cytokine) (TRANCE) (Osteoprotegerin ligand) (OPGL) (Osteoclast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "A homologic of the TNF receptor and its ligand enhance T-cell growth and dendritic-cell function."; Nature 390:175-179(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             225 SARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        257 GGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKV 312
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MEDLINE=98227661; PubMed=9568710; DOI=10.1016/S0092-8674(00)81569-X;
Lacey D.L., Timms E., Tan H.-L., Kelley M.J., Dunstan C.R.,
Burgess T., Elliott R., Colomboo A., Elliott G., Scully S., Hsu H.,
Sullivan J., Hawkins N., Davy E., Capparelli C., Eli A., Qian Y.-X.,
Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J.,
                                                                                                                                                                                                                                                                                                   65 WDP--NDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Osteoprotegerin ligand is a cytokine that regulates osteoclast differentiation and activation."; Cell 93:165-176(1998).
                                                                        51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM 1).
TISSUE-Bone marrow, and Peripheral blood;
MEDLINE-98032977; PubMed=9367155; DOI=10.1038/36593;
Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,
Tometsko M.E., Roux E.R., Teepe M.C., DuBose R.F., Cosman D.,
Galibert L.;
   DB 1; Length 316;
                                                                                                                                                     10 PSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACF
17.5%; Score 258.5; DB 1; Length 26.4%; Pred. No. 6.3e-13; ative 54; Mismatches 113; Indels
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"Determination of human RANKL isoforms.";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=TNFSF11; Synonyms=OPGL, RANKL, TRANCE;
Homo sapiens (Human).
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Ikeda T., Kuroyama H., Hirokawa K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM 1).
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                                                                        Conservative
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                                      Local Similarity
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       Query Match
                                                                        Matches
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                                                                                                                                                                                                                                                                                                                  Biochem. Biophys. Res. Commun. 269:532-536 (2000).

-!- FUNCTION: Cytokine that binds to TMRRSF11B/OPG and to TMRRSF11A/RANK. Osteoclast differentiation and activation factor. Augments the ability of dendritic cells to stimulate naive T-cell proliferation. May be an important regulator of interactions between T cells and dendritic cells and may play a role in the regulation of the T cell-dependent immune response. May also play an important role in enhanced bone-resorption in humoral hypercalcemia of malignancy.

-!- SUBGLIULAR LOCATION: Type II membrane protein (isoforms 1 and 3); Secreted (isoforms 2). A soluble form of isoform 1 arises by proteolytic processing (By similarity).
                                                            Choi Y.;
"TRANCE is a novel ligand of the tumor necrosis factor receptor family that activates c-Jun N-terminal kinase in T cells.";
J. Biol. Chem. 272:25190-25194(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isozda-014788-3; Sequence=VSP_006446;
TISSUE SPECIFICITY: Highest in the peripheral lymph nodes, weak in
spleen, peripheral blood Leukocytes, bone marrow, heart, placenta,
skeletal muscle, stomach and thyroid.
INDUCTION: Up-regulated by T cell receptor stimulation.
PTM: The soluble form of isoform I derives from the membrane form
by proteolytic processing. (By similarity). The cleavage may be
catalyzed by ADAMI?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and 3);
MEDLINE=97460112; PubMed=9312132; DOI=10.1074/jbc.272.40.25190;
Wong B.R., Rho J., Arron J., Robinson E., Orlinick J., Chao M.,
Kalachikov S., Cayani E., Bartlett P.S. III, Frankel W.N., Lee S.Y.,
                                                                                                                                                                                                                                      Nagai M., Kyakumoto S., Sato N., "Cancer cells responsible for humoral hypercalcemia express mRNA encoding a secreted form of ODF/TRANCE that induces osteoclast
                                                                                                                                                                                           TISSUE-Tongue;
MEDLINE=20175237; Pubmed=10708588; DOI=10.1006/bbrc.2000.2314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO; GO:0005887; C:Integral to plasma membrane; NAS.
GO; GO:0005164; F:tumor necrosis factor receptor binding; NAS.
GO; GO:0005164; F:tumor necrosis factor receptor binding; NAS.
GO; GO:0003016; P:seteoclast differentiation; NAS.
InterPro; IPR06652; TNF family.
InterPro; IPR068983; TNF like.
InterPro; IPR003636; TNF gubf.
Pfam; PF00229; TNF; INF gubf.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: Belongs to the tumor necrosis factor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Event=Alternative splicing; Named isoforms=3;
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Name=2; Synonyms=SODF;
IsoId=014788-2; Sequence=VSP_006447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30, GO:0005576, C:extracellular; NAS.
                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF019047; AAB86811.1; -. EMBL; AF053712; AAC39731.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, AB064269; BAB79694.1; --
EMBL, AB064227; BAB71768.1; --
EMBL, AB064270; BAB79695.1; --
EMBL, AR017171; AAC51762.1; --
EMBL, AB037599; BAA90488.1; --
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genew; HGNC:11926; TNFSF11.
MIM; 602642; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; 035235; 1JTZ.
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62 -DSYWDPNDEESMNSPCWQVKW-----OLRQLVRKMILRTSEETI-----STVQEKQ 107
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                                                                                                                                                                                                                                                          member 11, membrane form.

Tumor necrosis factor ligand superfamily member 11, soluble form (By similarity). Cytoplasmic (Potential).

Signal-anchor for type II membrane protein (Potential).

Extracellular (Potential).

Cleavage (By similarity).

N-linked (GlcNAc. .) (Potential).

N-linked (GlcNAc. .) (Potential).

Missing (in isoform 3).

/FILG-VSP 006446.

Missing (In isoform 2).
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                                                                                                                                                                                                                          Tumor necrosis factor ligand superfamily
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MEDLINE-94185175; PubMed=7511063; DOI=10.1016/0092-8674(94)90375-1;
Takahashi T., Tanaka M., Brannan C.I., Jenkins N.A., Copeland N.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Suda T., Nagata S.;
"Generalized Lymphoproliferative disease in mice, caused by a point
mutation in the Fas ligand.";
Cell 76:969-976(1994).
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
Tumor necrosis factor ligand superfamily member 6 (FAS antigen
SWART; SM00207; TNF; 1.
PROSITE; PSO0251; TNF_1: FALSE_NEG.
PROSITE; PSS0049; TNF_2; 1.
Alternative splicing; Cytokine; Differentiation; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 17.0%; Score 251.5; DB 1; Length 317; Best Local Similarity 24.1%; Pred. No. 2.4e-12; Matches 71; Conservative 61; Mismatches 117; Indels 45;
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A -> G (in Ref. 4).
766176446348097F CRC64;
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                                                                                                                                                                           Receptor; Signal-anchor; Transmembrane CHAIN 1 317 Tumor neco
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171
198
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CARBOHYD
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i- FUNCTION: Cytokine that binds to TWFRSP6/FAS, a receptor that transduces the apoptotic signal into cells. May be involved in cytotoxic T cell mediated apoptosis and in T cell development. TWFRSP6/FAS-mediated apoptosis may have a role in the induction of peripheral tolerance, in the antigen-stimulated suicide of mature T cells, or both. Binding to the decoy receptor TWFRSF6B/DcR3 modulates its effects (By similarity).
-i- SUBUNIT: Homotrimer (Probable).
-i- SUBCELLULAR LOCATION: Type II membrane protein (isoform FASL);
                                                                                                                                                    MEDLINE=95196085; PubMed=7889405; DOI=10.1016/1074-7613(94)90106-6; Lynch D.H., Wateson M.L., Alderson M.R., Baum P.R., Miller R.E., Tough T., Gibson M., Davis-Smith T., Smith C.A., Hunter K.; "The mouse Fas-ligand gene is mutated in gld mice and is part of a TNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isoid=P41047-2; Sequence=VSP 006445;
-!- PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).
-!- DISEASE: A deficiency in this protein is the cause of generalized lymphoproliferation disease phenotype (gld). Gld mice present lymphopropathy and autoantibody production. The phenotype is recessively inherited.
-!- SIMILARITY: Belongs to the tumor necrosis factor family.
                                                                                                                                                                                                                                                                                                                                                       Fenner M.H., Shioda T., Isselbacher K.J.;
"Mus musculus Balb/c Fas ligand differs from 129/SV Fas ligand in two
                       Peitsch M.J., Tschopp J.J.;
"Comparative molecular modelling of the Fas-ligand and other members
of the TNF family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Χ.
#EDLINE=95388076; PubMed=7544870; DOI=10.1016/0161-5890(95)00016-8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20021694; Pubmed=10552956;
Ayroldi E., D'Adamio F., Zollo O., Agostini M., Moraca R.,
Ayroldi E., D'Adamio F., Zollo O., Agostini M., Moraca R.,
Cannarile L., Migliorati G., Delfino D.V., Riccardi C.;
"Cloning and expression of a short Fas ligand: a new alternatively
spliced product of the mouse Fas ligand gene.";
Blood 94:3456-3467(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARIANTS ALA-184 AND GLY-218.
STRAIN-BALB/c, C3H, C57BL/6, DBA/1, DBA/2, MRL, NOD, NZB, NZW, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=97268671; PubMed=9108079; DOI=10.1073/pnas.94.8.3914;
Kayagaki N., Yamaguchi N., Nagao F., Matsuo S., Maeda H., Okumura
Yagita H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHARACTERIZATION OF VARIANT GLD.
MEDLINE=96091792; PubMed=7495745;
Hahne M., Peitsch M.C., Irmler M., Schroeter M., Lowin B.,
Rousseau M., Bron C., Renno T., French L., Tschopp J.;
"Characterization of the non-functional Fas ligand of gld mice.";
Int. Immunol. 7:1381-1386(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Polymorphism of murine Fas ligand that affects the biological
                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               activity.";
Proc. Natl. Acad. Sci. U.S.A. 94:3914-3919(1997).
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ALTERNATIVE PRODUCTS:
                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM FASL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM FASLS)
STRAIN=C3H; TISSUE=Spleen;
                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM FASL).
                                                                                   Mol. Immunol. 32:761-772(1995).
                                                                                                                                                                                                                                                                    [mmunity 1:131-136(1994).
                                                                                                                                                                                                                                               gene cluster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=FasLS;
                                                                                                                                                                                                                                                                                                                                       STRAIN=BALB/c;
                                                                                                                                                                                                                                                                                                                                                                                                           amino acids."
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use by non-profit institutions as long as its content is in no way andlified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83 QLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSK 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    111 ELREPTNQSL------NVSSFEKQIANPSTPSEKKEPRSV-AHLTG------NPHSR 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                143 NEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKN 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   203 DKQMVQYIY-KYTSYPDPILLMKSAR-NSCWSKDAEYGLYSIYQGGIFELKENDRIFVSV 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              L. s. cann DBA/2; enhances cytotoxicity).

E -> G (in strain BALB/c, strain DBA/1
and strain DBA/2; enhances cytotoxicity).

F -> L (in gld; abolishes binding of FASL
to its receptor).
                                                                                                                                                                                                                                                                                                                                                 Tumor necrosis factor ligand superfamily member 6, membrana form.

Tumor necrosis factor ligand superfamily member 6, soluble form (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              202 NQPLNHKVYMRNSKYPEDLVLMEEKRLNYCTT--GQIWAHSSYLGAVFNLTSADHLYVNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Missing (in isoform FasLS).
FTIdavSP 006445.
T -> A (in strain BALB/C, strain DBA/1
and strain DBA/2; enhances cytotoxicit;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                      Cytoplasmic (Potential).
Signal-anchor for type II membrane
protein (Potential).
Extracellular (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . .) (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 189.5; DB 1; Length 279;
Pred. No. 2.5e-07;
                                                                                                                                                                                                                                                                               Prodom; PD002012, TNF gubf; 1.
PROSITE; PS00451; TNF 1; 1.
PROSITE; PS0049; TNF 2; 1.
Alternative splicing; Apoptosis; Cytokine; Disease mutation; Glycoprotein; Polymorphism; Signal-anchor; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cleavage (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             279 AA; 31442 MW; 37972E2728E0A1CA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Potential.
N-linked (GlCNAc. .) (
N-linked (GlCNAc. .) (
N-linked (GlCNAc. .) (
N-linked (GlCNAc. .) (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Poly-Pro.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pro-rich
                                                          EMBL; U06948; AAA17800.1; --
EMBL; U10944; AAA17800.1; --
EMBL; S7675; AAB3780.1; --
EMBL; AF19335; AAB2915.1; --
EMBL; AF19335; AABC2916.1; --
EMBL; A53062; A53062.
HSSP; P50591; 1DG6.
MCD; MC1:99255; Thfsf6.
InterPro; IPR006064; Fas_ligand.
InterPro; IPR006053; TNF_abc.
InterPro; IPR006053; TNF_abc.
InterPro; IPR006053; TNF_abc.
InterPro; IPR008983; TNF_like.
InterPro; IPR03636; TNF_subf.
PRINTS; PR01681; FASLIGAND.
PRINTS; PR01681; FASLIGAND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        261 TNEHLIDMDHEASFFGAF 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          260 SQLSLINFEESKTFFGLY 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12.8%;
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                                                                                                                                                                                                                                                                                                                                                                              279
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100
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69
69
1128
231
117
117
1182
248
258
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45
127
200
200
117
182
248
258
258
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NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alderson M.,
                                                                                                                                                    61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  specificity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      infection.
                                                                                                                                                                                                                                                                                                                                    119
                    CARBOHYD
CARBOHYD
                                              CARBOHYD
                                                                SEQUENCE
                                                                                                             Query Match
                                                                                                                                      Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Cloning, sequencing, and homology analysis of nonhuman primate "Cloning, sequencing, and homology analysis of nonhuman primate Pas/Ras-ligand and co-stimulatory molecules.";

Immunogenetics 33:315-328 (2001).

Immunogenetics 33:315-328 (2001).

Immunogenetics 33:315-328 (2001).

Irmunogenetics 53:315-328 (2001).

Irmunogenetics 7:210 (2001).

Transduces the apoptotic signal into cells. May be involved in cytocoxic T cell mediated apoptosis and int T cell development.

TNFRSF6/FAS-mediated apoptosis may have a role in the induction of peripheral tolerance, in the antigen-stimulated suicide of mature T cells, or both. Binding to the decoy receptor TNFRSF6B/DCR3 modulates its effects (By similarity).

-!- SUBGNIT: Homotrimer (Probable).

-!- SUBGNIT: Homotrimer (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM0020/; INF 1; 1.
PROSITE; PS00251; TNF 1; 1.
PROSITE; PS0049; TNF 2; 1.
Apoptosis; Cytokine; Glycoprotein; Signal-anchor; Transmembrane.
Apoptosis; Cytokine; Glycoprotein; Signal-anchor; Transmembrane.
Tumor necrosis factor ligand superfamily member 6, membrane form.
                                                                                                        28-FEB-2003 (Rel. 41, Last sequence update)
55-JUL-2004 (Rel. 44, Last annotation update)
Lumor necrosis factor ligand superfamily member 6 (FAS antigen ligand)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tumor necrosis factor ligand superfamily member 6, soluble form (By similarity). Cytoplasmic (Potential).
                                                                                                                                                                                                                Cercocebus torquatus atys (Red-crowned mangabey) (Sooty mangabey) 
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, 
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae, 
Cercopithecinae, Cercocebus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Signal-anchor for type II membrane
                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Lymphocytes;
MEDLINE=21383618; PubMed=11491535; DOI=10.1007/s002510100322;
Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
Weiss W.R., Ansari A.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    proteolytic processing (By similarity).
-!- SIMILARITY: Belongs to the tumor necrosis factor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             similarity).
-!- PTM: The soluble form derives from the membrane form by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein (Potential).
Extracellular (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Poly-Pro.
Cleavage (By similarity).
Potential.
                                            280 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pro-rich
                                         PRT;
                                                                                                                                                                       (CD95L protein).
Name=TNFSF6; Synonyms=CD95L, FASL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF344847; AAK37606.1; -. HSSP; P50591; 1D20.
InterPro; IPR008064; Fas ligand.
InterPro; IPR006053; TNF_abc.
InterPro; IPR006052; TNF_family.
InterPro; IPR008983; TNF_like.
InterPro; IPR003636; TNF_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PRO1681; FASLIGAND.
PRINTS; PRO1234; TWECROSISFCT.
PRODOM; PRO02012; TNF 8UDE; 1.
SMART; SM00207; TNF; 1.
                                                                                     (Rel. 41, Created)
                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101
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64
232
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9531;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45
128
201
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                                                                                 28-FEB-2003
28-FEB-2003
                                                                                                                               05-JUL-2004
                                       CERTO
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DISULFID
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                                                          Q9BDN1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----QKHTASSLEKQIGHPSP-PPEKKEÖRKV 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124 AHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFYY 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                146 AHLTG------KPNSRSMPL-----EWEDT-YGIVLLSGVKYKKGGLVINETGLYF 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            184 IYSQTYFRFQEEIKENTKNDKQMVQYIY-KYTSYPDPILLMKSARNSCWSKDAEYGLYSI 242
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P48023; Q9BZP9;
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Tumor necrosis factor ligand superfamily member 6 (FAS antigen ligand)
(Apoptosis antigen ligand) (APTL) (CD178 antigen).
Name=TWRSF6; Synonyms=APTLLG1, FASL;
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                            4 MEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKEDDS
                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM 1).
MEDILINE-95127560; PubMed=7826947;
Takahashi T., Tanaka W. Inazawa J., Abe T., Suda T., Nagata S.;
"Human Fas ligand: gene structure, chromosomal location and species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-95071350; PubMed-7980502; Mitta E., Hayashil N., Ito S., Takehara T., Hijioka T., Kasahara A., Fusamoto H., Kamada T.; Rapeda T.; Role of Fas ligand in apoptosis induced by hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
(GlcNAc. . .) (Potential) (GlcNAc. . .) (Potential) (GlcNAc. . .) (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fas ligand mediates activation-induced cell death in human T
                                                                                                                                                    DB 1; Length 280;
                                                                                                                                                                                                                91; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM 1).
Schaetzlein C.E., Poehlmann R., Philippsen P., Eibel H.;
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
N-linked (GlcNAc. . .) (Pc
N-linked (GlcNAc. . .) (Pc
N-linked (GlcNAc. . .) (Pc
729EA60067B7D398 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       243 YLGAVFNLTSTDHLYVNVSELSLVNFEESQTFFGLY 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biochem. Biophys. Res. Commun. 204:468-474(1994)
                                                                                                                                                                                    4e-07;
                                                                                                                                                                                                                56; Mismatches
                                                                                                                                                 12.7%; Score 187; 22.1%; Pred. No. 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=95105731; PubMed=7528780;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nt. Immunol. 6:1567-1574(1994).
183 N-
249 N-
259 N-
31407 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM 2)
TISSUE=Leukocyte;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Exp. Med. 181:71-77(1995).
                                                                                                                                                                                                                Conservative
183
249
259
280 AA;
                                                                                                                                                                                 Similarity
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REDLINE=22388257; PubMed=12477912; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.N.,
A Altschul S.F., Zeeberg B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Brownstein M.J., Ugdin T.B., Toobhlyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McKennan F.J., McKernan K.J., Malek J.A., Gunarane P.H.,
Richards S., Worley K.C., Hale S., Garcha A.M., Gay L.J., Hulyk S.W.,
A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.B.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.B.,
Brownstein A., Schmit J., Marra M.A.,
Brownstein A., Schmit J., Brownstein B., Marra M.A.,
Brownstein A., Schmit J., Brownstein B., Marra M.A.,
Brownstein A., Schmit J., Brownstein B., Marra M.A.,
Brownstein A., Schmit J., Br
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Tanaka M., Itai T., Adachi M., Nagata S.;
Tanaka M., Itai T., Adachi M., Nagata S.;
Tanaka M., Itai T., Adachi M., Nagata S.;
Powntegulation of Fas ligand by shedding.";
Nat. Med. 4:31-36(1998).

-!- FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that transduces the apoptotic signal into calls. May be involved in cytotoxic T cell mediated apoptosis and in T cell development.

TNFRSF6/FAS-mediated apoptosis may have a role in the induction of peripheral tolerance, in the antigen-stimulated suicide of mature T cells, or both. Binding to the decoy receptor TNFRSF6B/DCR3 modulates its effects.

-!- SUBUNIT: Homotrimer (Probable).
                                 οĘ
Zeytun A., Nagarkatti M., Nagarkatti P.S.;
"IsoJation and characterization of a new naturally occuring variant
human Fas ligand that is expressed only in membrane bound form.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
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DISBASE: Defects in TNRSF6 are a cause of autoimmune
lymphoproliferative syndrome (ALPS) [MIM:601859]; also known as
Canale-Smith syndrome (CSS). ALPS is a childhood syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHARACTERIZATION, AND MUTAGENESIS OF PRO-206; TYR-218 AND PHE-275. MEDLINE=97373583; PubMed=9228058; DOI=10.1074/jbc.272.30.18827; Schneider P., Bodmer J.-L., Holler N., Mattmann C., Scuderi P., Terskikh A., Peitsch M.C., Tschopp J.; "Characterization of Fas (Apo-1, CD95)-Fas ligand interaction."; J. Biol. Chem. 272:18827-18833(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matsumura M., Nakanishi Y., Ohba Y.;
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                         Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM 1).
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                                                                                                                                               SEQUENCE FROM N.A.
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R GO; GO:0005887; C:integral to plasma membrane; TAS.
R GO; GO:0005887; C:integral to plasma membrane; TAS.
R GO; GO:0005102; F:receptor binding; TAS.
R GO; GO:0007267; F:cell-cell signaling; TAS.
R GO; GO:0006917; P:induction of apoptosis; TAS.
R GO; GO:0007165; F:signal transduction of I-kappaB kinase/NF-k. .; IEP.
R GO; GO:0007165; F:signal transduction; TAS.
R InterPro; IPR008064; Fas ligand.
R InterPro; IPR008065; TNF-abc.
R InterPro; IPR008083; TNF-like.
R InterPro; IPR008983; TNF-like.
R PRINTS; PR01691; FASIIGAND.
R PRINTS; PR01691; FASIIGAND.
                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tumor necrosis factor ligand superfamily member 6, membrane form.

Tumor necrosis factor ligand superfamily member 6, soluble form.
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/FTId=VSP_006444.
P->D,F,R: Lowers binding to TNFRSF6 and
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STSQMHTASSL -> ATPVHPLKKRS (in isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           abolishes cytotoxity. F->L: Abolishes binding to TNRFSF6 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 reduces cytotoxity more than 100-fold. Y->F,R: Lowers binding to TNFRSF6 and
             lymphadenopathy and splenomegaly. SiMiLARITY: Belongs to the tumor necrosis factor family. DATABASE: NAME=PROW 2:59-69(2001); WWW="http://www.ncbi.nlm.nih.gov/prow/guide/333879674_g.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ProDom; PD002012; TNF subf; 1.
PROSITE; PS00251; TNF 1; 1.
PROSITE; PS50049; TNF 2; 1.
Alternative splicing; Antigen; Apoptosis; Cytokine; Glycoprotein;
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N-linked (GlCNAc. ..) (Potential).
N-linked (GlCNAc. ..) (Potential).
N-linked (GlCNAc. ..) (Potential).
involving hemolytic anemia and thrombocytopenia with massive
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Extracellular (Potential).
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EMBL; U1821; AACS0024.1; -
EMBL; D38122; BAA07320.1; -
EMBL; AF288673; AAG60017.1; -
EMBL; 296050; CAB09424.1; -
EMBL; AB01303; AAH17502.1; -
EMBL; AB01303; BAA32542.1; -
FIR; 138707; 138707.
HSSP; P50591; 1D20.
Genew; HGNC:11936; TNFSF6.
H-INVDB; HIX0001337; -
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                                                                                                                                                             A novel cytokine (AAW19777), designated Apo-2 ligand, induces mammalian cell apoptosis. It is belived to be a member of the tumour necrosis factor cytokine family. Its amino acid sequence was deduced from a cDNA clone (AAT72796) isolated from a human placental cDNA library. Apo-2 ligand polypeptides, esp. those corresponding to amino acids 114-281, 41-281, 15-281 or 1-281 of Apo-2 ligand, can be produced by culturing cells transformed or transfected with a vector contg. Apo-2 ligand nucleic acid. They can be used to induce apoptosis in mammals and to treat pathological conditions such as cancer (esp. breast or colon cancer) or to raise antibodies useful in diagnostic assays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FYX I YSQTYFRFQEEI KENTKNDKQWVQY I XKYTSYPDPILLMKSARNSCWSKDAEYGLY
                                                                                                                                                                                                                                                                                                                                                                            1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
                                                                                                                                                                                                                                                                                                                                                                                                  DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                             RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY
                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Apoptosis inducing molecule-I; AIM-I; autoimmune disorder; tumour necrosis factor ligand superfamily; AIM-I altered expression; neoplasia inhibition; anti-inflammatory agent.
                                                                                                        Novel cytokine, Apo-2 ligand and corresponding DNA - used to induce apoptosis for the treatment of breast and colon cancer.
                                                                                                                                                                                                                                                                                                                                  0,
                                                                                                                                                                                                                                                                                                          100.0%; Score 1478; DB 2; Length 281; 100.0%; Pred. No. 3.8e-137; ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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                                                     Kim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW27134 standard; protein; 281 AA
                                                                                                                                          Claim 4; Fig 1a; 72pp; English.
                                                   Chuntharapai A,
         96US-00584031
                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
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                               (GETH ) GENENTECH INC
                                                                         WPI; 1997-372867/34.
N-PSDB; AAT72796.
                                                                                                                                                                                                                                                                                      Sequence 281 AA;
                                                     Ashkenazi AJ,
         09-JAN-1996;
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The present sequence represents a human Apoptosis inducing molecule-I (AIM-I). AIM-I is a member of the tumour necrosis factor (TNF) ligand superfamily. The products can be used in the diagnosis and treatment of disorders related to under-expression, over-expression or altered expression of AIM-I. AIM-I or agonists can be used for treating autoimmunoproliferative disease lymphadenopathy (IPL), rheumatosus, immunoproliferative lymphadenopathy (IPL), rheumatoid arthritis, angioimmunoproliferative lymphadenopathy (AIL), rheumatoid arthritis, compandats auto as tumour call growth, to treat restenosis, to regulare haematopoiseis in endothelial call development, to stimulate peripheral tolerance and cytotoxic T-cell mediated apoptosis. Antagonists can be used for treating cachexia, cerebral malaria, rheumatoid arthritis or settoporosis, for preventing graft-host rejection, and as anti-illammatory agents, for treating endotoxic shock or to prevent
                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated apoptosis inducing molecule-I - used to develop products for
the diagnosis and therapy of e.g. autoimmune diseases, tumours, graft
versus host disease or inflammation.
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cytokine; cancer; leukaemia; lyphoma; melanoma; viral infection;
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100.0%; Pred. No. 3.8e-137;
ive 0; Mismatches 0;
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96WO-US003773.
                                                                      96WO-US003773
                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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Matches 281; Conservative
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N-PSDB; AAT85210.
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120 180 180 240 240

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121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG
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97US-00853684.
97US-00916625.
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                                                                                                                                                         (first entry)
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N-PSDB; AAV63096.
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                                                                                                                                                                                       Human TL2 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 281 AA;
                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                          23-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                    14-MAR-1997;
09-MAY-1997;
                                                                                                                                                         25-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-AUG-1997,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Simines 281;
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                                                                                                                              AAW76829;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human tumour necrosis factor related apoptosis inducing ligand (TRALL) (AAM19787) is a novel cytokine that induces apoptosis of certain target cells, including cancer cells and virally infected cells. Its amino acid sequence was deduced from cDNA clone HuAIC (AA772848), deposited in vector pDC409 as ATCC 69849. Recombinant TRALL polypeptides (esp. soluble polypeptides) can be expressed in host cells and used in the treatment of cancer (e.g. leuksemia, lymphoma and melanoma) and viral infections, or to raise antibodies that may be useful for treating thrombotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLIMKSARNSCWSKDAEYGLY 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , a novel cytokine, induces apoptosis in cancer and virus-infected - useful for treating thrombotic microangiopathy, cancer and viral
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                                                                                                                                                                                       site"
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                                                                                                                                                        'note= "contains a receptor-binding region"
                                                                                                                                                                                       'note= "potential KEX2 protease processing
                                                                                                                                                                                                                                             /note= "potential KEX2 protease processing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                  /note= "potential N-glycosylation site"
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                                                                                                   19. .38
/label= Transmembrane_domain
                                                                                                                              39. .281
/label= Extracelular_domain
                                                                     1. .18
/label= Cytoplasmic_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
thrombotic microangioplasty; therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 10; Page 43-44; 62pp; English.
                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       infection and for use in assays.
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95US-00548368.
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                                                                                                                                                                                                                                                                                                                                                                                                          (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1997-118715/11.
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                                                                                                                                                                       Cleavage-site
                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                Cleavage-site
                            Homo sapiens
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Best Local Simi
Matches 281;
                                                                                                                                                                                                                                                                            WO9701633-A1
                                                                                                                                                                                                                                                                                                                                   25-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                              29-JUN-1995;
                                                                                                                                                                                                                                                                                                       16-JAN-1997
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This sequence represents the human tumour necrosis factor (TNF)-related receptor, TL2 (also known as tumour necrosis factor-related apoptosis-inducing ligand, TRAIL). This protein is used in a method resulting in polyapetides and polynucleotides can be used in the treatment of the novel human TNF related receptor, TR6. TR6 polyapetides and polynucleotides can be used in the treatment of chronic and acute inflammation, arthritis, septicaemia, autoimmune diseases (e.g. inflammatory bowel disease, psoriasis), transplant rejection, graft vs. host disease, infaction, stroke, ischaemia, acute respiratory disease syndrome, restenosis, brain injury, (acquired autoimmune disease syndrome) alds, bone disease, cancer (e.g. lympho-proliferative disorders), atherosclerosis and Alzheimers disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TR6; tumour necrosis factor related receptor; human; treatment; stroke; inflammation; arthritis; septicaemia; autoimmune disease; restenosis; transplant rejection; infection; ischaemia; brain injury; bone disease; acute respiratory disease syndrome; acquired autoimmune disease syndrome; AIDS; cancer; atherosclerosis; Alzhaimers disease; TRAIL; TNF; TL2. tumour necrosis factor-related apoptosis-inducing ligand.
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100.0%; Pred. No. 3.8e-137;
ive 0; Mismatches 0;
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DDSYMDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120

DDSYWDPNDEESMINSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ

RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180

121

181 181

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RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG

SIYQGGIFELKENDRIFVSVINEHLIDMDHEASFFGAFLVG 281 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

241

241

AAW44354 standard; protein; 281

(first entry)

28-MAY-1998

AAW44354;

Human AGP-1.

FYY I YSQTYFRFQEEI KENTKNDKQMVQY I YKYTSYPDPI LLMKSARNSCWSKDAEYGLY

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Tumour necrosis factor related apoptosis ligand; TRAIL; research; human;
cytokine; therapy; leukaemia; lymphoma; melanoma; viral infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA encoding cytokine TNF-related apoptosis ligand polypeptides - useful for producing recombinant polypeptides for research and therapy of leukaemia, lymphoma, melanoma and viral infections.
                               FYYIYSQTYFRFQEBIKENTKNDKQMVQYIYKYTSYPDFILLMKSARNSCWSKDAEYGLY
                                           181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY
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                                                                       SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
                                                                                  241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
                                                                                                                                                                                                                                                                                                "N-terminal cytoplasmic domain"
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                                                                                                                                                                                                                                                                                                                    "transmembrane region"
                                                                                                                                                                                                                                                                                                                                        "extracellular domain"
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95US-00548368.
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Human; AGP-1; tumour necrosis factor-related protein; TNF; inflammation; bone resorption; haematopoietic disease.

Homo sapiens

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The present sequence represents human AGP-1. AGP-1 is a tumour-necrosis factor (TNF)-related protein, involved in inflammation, myelopoiesis and bone resorption. It has the same nucleic acid and amino acid (aa) sequences as the TNF-related apoptosis-induced ligand (TRAIL) described in Immunity, 3 (1995) 673. Antibodes (Ab) are used as immunoassay reagents for detecting AGP-1 expression. Nucleic acid complementary to AGP-1 is used to requiate AGP-1 expression and antagonistic compounds are used to treat inflammation (e.g. rheumatoid arthritis, systemic lupus erythematosus, psoriasis, scleroderma, infection-related inflammation) or one resorption diseases (e.g. osteopyzoals, osteomyzolitis, chaematopoietic diseases associated with reduction in the number of bone marrow cells, particularly neutrophils and lymphocytes, e.g. where caused by disease, injury or exposure to myelosuppressive agents. Host cells, transformed with expression vectors containing AGP-1 DNA, are used to produce recombinant AGP-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid encoding AGP-1, a tumour necrosis factor-related protein useful for treating inflammation, bone resorption and haematopoietic
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WO9746686-A2
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Gaps

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Sequence 281 AA;
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                                                                                                                                                                                                                                                                                                    RVAAHITGTRGRSNTLSSPNSKAEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
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                                                                                                                    1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
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                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neurodegenerative disease; autoimmune disease; inflammatory disease; lupus erythematosus; rhuematoid arthritis; SEP; apoptotic; surface receptor; TRAIL protein.
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                                     Length 281;
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                                     Score 1478; DB 2;
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                                       100.0%;
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  Sequence 281 AA;
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anti-TRAIL antibody or a TRAIL equivalent that binds to specific receptors, inhibiting formation of natural complex
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                                                                                                                                              Length 281;
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                                                                                                                                        ; Score 1478; DB 2;
; Pred. No. 3.8e-137;
0; Mismatches 0;
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                                                                                                                                              100.0%;
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in mammalian cancer cells.
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                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 281, Conservative
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N-PSDB; AAX86987.
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n quantitative and screening diagnostic can be used for treating diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence is the human Apo-2 ligand protein, which is recognised by monoclonal antibodies produced by the hybridoma cell lines of the invention. The hybridoma cell lines are deposited under the American Type Culture Collection Accession Numbers: ATCC HB-12256, HB-12257, HB-12258 and HB-12259. The Apo-2 ligand antibodies may be used in diagnostic
                                                                                                                                                                                                                            DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
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                                                                                                                                                                                                                                                                                 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
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coding sequence can also be used in techniques. Anti-Apo-2L antibodies associated with increased apoptosis
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Best Local Similarity 100.
Matches 281; Conservative
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N-PSDB; AAA07425.
                                                        Sequence 281 AA;
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assays for Apo-2 ligand, e.g. detecting its expression in specific cells, tissues, or serum. The antibodies may also be employed as therapeutics. For instance, anti-Apo-2 ligand antibodies which block Apo-2 ligand activity, like Apo-2 ligand-induced apoptosis, may be employed to treat pathological conditions or diseases associated with increased apoptosis. They are also useful for the affinity purification of Apo-2 ligand from recombinant cell culture or natural sources. The Apo-2 ligand itself may be used to treat diseases e.g. cancer, by inducing apoptosis in cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WI;
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                                                                                                                                                                                                                                                                                                                         Length 281;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human PRO1096 protein sequence SEQ ID NO:51
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99US-0162506P.
99WO-US028313.
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N-PSDB; AACS8120.
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29-OCT-1999;
30-NOV-1999;
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                                             The present invention describes an antibody that binds to a human protein (I) selected from: PRO1381; PRO1269; PRO1410; PRO1755; PRO1780; PRO3341; PRO4357; PRO1295; PRO1295; PRO1295; PRO1295; PRO1295; PRO2295; PRO3303; PRO4407; PRO4555; PRO1096; PRO2058; and PRO2262; (I) has anticancer activity and can be used to diagnose tumours in mammals, by detecting complex formation when the antibody is contacted with test cells.

Increased expression of genes encoding (I) can also be detected to diagnose tumours. Agents which inhibit the activity of (I), especially the antibodies, or an antisense oligonucleotide which hybridises to genes encoding (I), can be used to inhibit tumour growth, preferably by inducing cell death. Methods from the present invention can be used to identify compounds which inhibit the biological activity of (I). AAC58019 to AAC58102 represent PCR primers and hybridisation probes used in the AAC5812 and AAB34021 to AAC58102 represent invention for human PRO sequences. AAC58101 to AAC5812 to AAC5
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100.0%; Pred. No. 3.8e-137;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Amino acid sequence of a human TRAIL polypeptide.
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                61; Fig 36; 226pp; English
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Matches 281; Conservative
                                                                                                                                                                                                                                                                                                                                                               Sequence 281 AA;
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Best Local S
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The present sequence represents a human TRAIL (tumour necrosis factor (TNF) related apoptosis-inducing ligand) polypeptide. The specification describes a method for enhanced killing of tumour cells. The method comprises contacting a susceptible tumour cell with a symergistic mixture of a TRAIL receptor ligand and a diterpenoid triepoxide in a combined dosage to kill at least 50 % of the cells. This mixture is symergistic, and so is active at lower doses and against otherwise resistant cell lines. The method is used for killing tumour cells, especially solid tumours or carcinomas (especially mammary carcinoma or non-small cell
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                                                                                                                                                 Killing of tumor cells, e.g. solid tumors or carcinoma, comprises administration of synergistic combination of diterpenoid diepoxide and tumor necrosis factor related apoptosis-inducing ligand.
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100.0%; Pred. No. 3.8e-137;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                        Disclosure; Page 23-24; 29pp; English.
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Best Local Similarity 100.
Matches 281; Conservative
                                                            WPI; 2000-558253/51
                                                                                              N-PSDB; AAA64325
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Rosen GD;
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Gurney AL, H
Watanabe CK,
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2000WO-US006884.
2000WO-US008439.
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2000WO-US005841.
2000US-0187202P.
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99US-0162506P
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Matches 281; Conservative
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11-FEB-2000; 2
18-FEB-2000; 2
18-FEB-2000; 2
02-MAR-2000; 2
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01-DEC-1999;
 07-DEC-2000
                                                                       23-JUN-1999
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                                                                                                                                                                             The present sequence is human AGP-1, a type II transmembrane protein. Fusion proteins comprising an FC immunoglobulin region fused to the Neterminal portion of the AGP-1 protein have been produced. The fusion proteins can be used to induce apoptosis in a tissue, and to treat proliferative disorders, immune disorders, or virally-induced disorders. The proliferative disorders include cancers, such as breast, prostate, lung or colon cancer. The viral infections include hepatitis, and acquired immunodeficiency syndrome (AIDS), and the immune disorders may be autoimmune disorders or transplant rejection. Cardiovascular diseases such as arteriosclerosis may also be treated. The AGP-1 containing fusion proteins used in prior art therapies
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                                                                                                                    Fusion protein of AGP-1 protein and an Fc region, used to treat proliferative disorders, immune disorders, and virally-induced disorders.
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antiinflammatory; antiangiogenic; immunosuppressive; immunostimulant;
PRO agonist; cancer; inflammatory disorder; immunological disorder.
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                                                                                                                                                        Claim 3; Fig 2; 93pp; English.
           99US-00293245
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Matches 281; Conservative
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N-PSDB; AAC67831.
                                   (AMGE-) AMGEN INC.
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           16-APR-1999;
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Hebert C, Henzel W, Kabakoff RC; , Wood WI;

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                                                                                                                                                                                                                                   The present sequence is one of twenty eight novel PRO polypeptides. The PRO polypeptides and their agonists, including antibodies, peptides, and small molecule agonists, may be used to treat various tumours, e.g., cancers such as breast cancer, ovarian cancer, renal cancer, colorectal cancer, uterine cancer, prostate cancer, lung cancer, bladder cancer, central nervous system cancer, melanoma or leukaemia. They are also useful for treating other disorders such as neuronal, glial, astrocytal, hypothalamic and other glandular, macrophagal, epithelial, stromal and blastocoelic disorders, and inflammatory, angiogenic and immunological
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Twenty eight nucleic acids encoding PRO polypeptides which are useful treating various tumors, e.g. breast cancer, and other inflammatory, angiogenic and immunological disorders.
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100.0%; Pred. No. 3.8e-137;
ive 0; Mismatches 0;
                                                                                                                                                                  Claim 31; Fig 54; 188pp; English
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Similarity
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Best Local Simi
Matches 281;
                                                                                                                                                                                                                                                                                                                                                                10-NOV-1998;
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25-JUN-1996;
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                                                         AAE11031;
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Domain
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181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
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                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to a formulation comprising Apo-2 ligand and divalent metal ions. Apo-2 ligand and the formulation are useful for treating cancers and viral infections. Addition of divalent metal ions for making Apo-2 ligand and formulations containing Apo-2 ligand results in increased yield and stability of Apo-2 ligand trimers
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                                                                                                                                                                                                                                                                                                                                                     Use of divalent metal ions for making Apo-2 ligand and in formulations containing Apo-2 ligand for increasing Yield and stability of ligand trimers, useful for therapeutic applications.
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                                                                                                                                                                                                                                                                                                         Leung
                                                                                                                                                                 divalent metal ions; viral infection;
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                             SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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                   SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG
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Shahrokh Z,
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                                                                                     AAB67243 standard; protein; 281
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                                                                                                                                                                                     Homo sapiens.
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O'connell
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The invention relates to a cytokine designated as tumour necrosis factor (TNF) related apoptosis inducing ligand (TRAIL), which induces apoptosis of certain target cells, including cancer cells and virally infected cells. The TRAIL polypeptides are useful in killing cancer cells, in treating viral infections (e.g. bovine viral diarrhoea or human immunodeficiency virus (HIV)) and cancers (e.g. leukaemia, lymphoma and melanoma), as a research reagent useful in studying apoptosis including the regulation of programmed cell death. TRAIL DNA sequences may be employed in developing a gene therapy approach to treating disorders mediated by defective or insufficient amounts of TRAIL, in the production of TRAIL polypeptides and as probes or primers in polymerase chain reactions (PCR). The present sequence is human TRAIL protein
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                                                                                                                                                                                                                                                                         Human; tumour necrosis factor; TNF; cytokine; cytostatic; virucide; TNF related apoptosis inducing ligand; TRAIL; cancer; viral infection; human immunodeficiency virus; HIV; leukaemia; gene therapy; lymphoma;
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                                                                                                                                                                                                          Human TNF related apoptosis inducing ligand (TRAIL) protein.
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'label= N_terminal_cytoplasmic_domain
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llarity 100.0%; Pred. No. 3.8e-137;
Conservative 0; Mismatches 0;
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AAE11031 standard; protein; 281
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98US-00048641.
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                                       DDSYWDPNDEBSWNSPCWQVKWQLRQLVRKMILRTSBETISTVQEKQQNISPLVRERGPQ 120
                        DDSYMDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
                                                                          RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New tumor necrosis factor related receptor TR6 polynucleotides and polypeptides useful for e.g. for treating chronic and acute inflammation, arthritis, septicemia, autoimmune diseases, infection, cancer, bone
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                                                                                                                                                                                                                                                                                                                                                               Tumour necrosis factor; TNP; TNF related receptor; TR6; human; TL2; antiinflammatory; immunosuppressive; cerebroprotective; vasotropic; antiasthmatic; anti-HIV; osteopathic; cytostatic; antiatherosclerotic; nootropic; neuroprotective; antiarthritic; antirheumatic; antiischemic; gene therapy; vaccine; TNF-alpha; bone disease; cancer; TRAIL.
                                                                                         MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
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                                                                                                                                                                                                                                                                AAB48350 standard; protein; 281
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                                                                                                                                                                                                                                                                                                                                        Human TL2 polypeptide.
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genes having high sequence similarity to TR6 gene, and for chromosome identification. The present sequence represents a human TL2 polypeptide. TL2 is also known as TRAIL (TNF-related apoptosis-inducing ligand) and is ligand for the TL2 polypeptide.
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Pred. No. 3.8e-137;
Mismatches 0;
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                                                                                                                                                                                                                                Similarity
                                                                                                                                               281 AA;
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Thomas EK;
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(a) dendritic cell mobilisation factor; (b) dendritic cell maturation agent; (c) dendritic cell activation agent; (d) T cell enhancing factor; or (e) activated, antigen-specific Tealls. The methods are useful for treating an individual at risk for or suffering from infection with a pathogenic or opportunistic organism, e.g. viruses (e.g. HIV), bacteria (e.g. M. tuberculosis), yeast, fungi (e.g. C. albicans) or protozoa (e.g. T. cruzi, which causes Chaga's disease). The methods are especially useful for treating an individual suffering from immunosuppression by enhancing a lymphocyte-mediated immune response. In particular, the method is useful for treating inflammations, chickenpox, oral or genital herpes, mononucleosis, multifocal leukencephalopathy, hepatitis, AIDS, T cell leukemia or T cell lymphoma. The activated antigen presenting dendritic cells are useful as a vaccine adjuvant. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DDSYWDPNDEESMNSPCWQVKWQLKQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
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                                                                                                                                                                                                                                                                                                                  100.0%; Score 1478; DB 5; Length 281; 100.0%; Pred. No. 3.8e-137;
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                                                                                                                                                                                                                                          represents a human TRAIL polypeptide fragment
                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                      281; Conservative
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                                                                                                                                                                                                                                                                                 Sequence 281 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to a new method for treating a tumourbearing subject. The method involves administering a combination of 2 to 5 agents comprising dendritic cell mobilisation factor, dendritic cell maturation agent, tumour-killing agent, T cell enhancing factor or activated, antigen-specific T cells. The method is useful for treating tumours or cancers in a subject e.g. skin cancer, prostate cancer, liver cancer, tumours of the bone, brain or spinal cord, actinic keratosis, or cervical intraepithelial neoplasia. The present amino acid sequence in the human TRAIL protein that was used in the method of the
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                                   Treating an individual with tumors or cancers, e.g. liver cancer or b tumor, by administering a combination of dendritic cell populations, cell enhancing factors and activated, antigen-specific T cells.
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                                                                                                              Disclosure, Page 41-43; 44pp; English
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Matches 281; Conservative
WPI; 2002-674891/72.
                                                                                                                                                                                                                                                                                                                                                               Sequence 281 AA;
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                                                                                                                                                                                                  This invention relates to a novel method for enhanced killing of tumour cells comprising contacting a tumour cell with a synergistic combination of a death domain receptor ligand and a diterpenoid triepoxide. This method has cytostatic activity and works by blocking TNF-alpha mediated induction of c-IAP2 and c-IAP1. The method of the invention may be used for treating tumours, particularly solid tumours, e.g. carcinoma, mammary adenocarcinoma and non-small cell lung carcinoma also neurological malignancies, haemacological malignant cutaneous T-cells, mycosis chronic lymphocytic leukaemia, malignant cutaneous T-cells, mycosis fungoides, non-MF cutaneous lymphoma, T-cell lymphoma, lymphomatoid papulosis, T-cell rich cutaneous lymphoid hyperplasia, bullous pemphigoid, discoid lupus erythematosus, lichen planus. The combination may be administered with other active agents, e.g. anti-metastatic, anti-tumour or anti-captive agents. The potent synergy between the diterpenoids and the death domain ligands allows increased killing at equivalent or lower construction and construction sequence. TRAIL is a death domain receptor used in the used construction in combination with diterpenoid triepoxides to with contents invention in combination with diterpenoid triepoxides to
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                                                                                                                                         Use of a synergistic combination of death domain receptor ligands and diterpenoid triepoxides for killing of tumor cells.
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Pred. No. 3.8e-137;
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                                                  (STRD ) UNIV LELAND STANFORD JUNIOR
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tive 0; 1
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                                                                                                  WPI; 2002-121125/16.
N-PSDB; ABK13192.
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Best Local Similarity
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          16-FEB-1999;
20-AUG-1999;
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                                                                           Rosen GD,
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The present sequence is that of human Apo-2 ligand (Apo-2L or TRAIL). The invention relates to methods of inducing apoptosis in mammalian cells, and despecially to the use of Apo-2L receptor agonists and CPT-11 (a chemotherapeutic agent of the topolsomerase I inhibitor class) to synergistically induce apoptosis in mammalian cells, in particular amammalian cancer cells, and sepecially colorectal cancer cells (laimed). The cells may be in cell culture or in a mammal, e.g. a mammal suffering from cancer or a condition in which induction of apoptosis in the cells administering CPT-11 and Apo-2L receptor agonist, where the CPT-11 is administered about 6-72 hours prior to administration of the Apo-2L receptor agonist. Preferred Apo-2L receptor agonist. Preferred Apo-1L receptor agonist. Preferred Apo-1L receptor agonist. Preferred Apo-1L receptor agonist leads to upregulation of DR4 and DR5 receptors. C canti-DR5 receptor agonist leads to upregulation of DR4 and DR5 receptors. C anti-DR5 receptor agonist leads to upregulation of DR4 and DR5 receptors. C arcest and possible DNA repair, thus providing enhanced antitumour cultumour growth by Apo-2L and CPT-11 in athymic nucle mijected s.c. with human colloss colon carcinoma cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 240
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Apo-2 ligand; Apo-2L; TRAIL; human; apoptosis; colorectal cancer; tumour; antitumour; therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Use of CPT-11 which is a chemotherapeutic agent of the topoisomerase I inhibitor class, and Apo-2 ligand receptor agonist for enhancing apoptosis in mammalian cells, or for treating cancer in a mammal.
                                                                                                                                                                                                                                    /note= "Apo-2L polypeptide used in method of Claim 18"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 18; Page 79-80; 84pp; English.
                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kelley SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                     27-JUL-2001; 2001WO-US023691.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Escandon E, Fox JA,
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                                                                                                                                                                                                                                                                                                      WO200209755-A2
                                                                                                     Homo sapiens
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                                                                                                                                                                                                    Protein
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The present invention describes an Escherichia coli strain (I) deficient in chromosomal degp and prc encoding protease Degp and Prc, respectively, and harbouring a mutent spr gene, the product of mutant spr gene suppresses growth phenotypes exhibited by strains harbouring prc mutants.

(I) is useful for producing a polypeptide, by culturing (I) comprising nucleic acid encoding the polypeptide, which is heterologous to the strain, such that the nucleic acid is expressed, and recovering the strain, such that the nucleic acid is expressed, and recovering the terrologous polypeptide from the strain. The heterologous polypeptide is proteolytically sensitive. Culturing of (I) is performed in a fermentor under conditions of high- or low-cell density fermentation. The polypeptide is an antibody (humanised or full-length antibody) or Apo2 ligand. The antibody is an anti-tissue factor, 2C4, anti-Her-2, anti-CD20, anti-CD40, or anti-CD10 antibody is also an antibody fragment having a light chain (kappa light chain). The antibody fragment having a light chain (kappa light chain). The antibody fragment having a light chain (kappa light chain). The antibody fragment sea Pab, Fab, Fab, Pab, 2 or Fab/2-leucine zipper fusion, anti-Lissue factor Fab/2-leucine zipper fusion with a 6-histidine tag, anti-CD18 (Fab/2-leucine zipper fusion with a 6-histidine tag, and anti-CD18 (Fab/2-leucine zipper fusion with a 6-histidine tag, and anti-CD18 (Fab/2-leucine zipper fusion with a 6-histidine tag, and anti-CD18 (Fab/2-leucine zipper fusion with a 6-histidine tag, and anti-CD18 (Fab/2-leucine zipper fusion with a 6-histidine tag, and anti-CD18 (Fab/2-leucine zipper fusion with a 6-histidine tag, and anti-CD18 (Fab/2-leucine zipper fusion with a 6-histidine tag, and anti-CD18 (Fab/2-leucine zipper fusion with a 6-histidine tag, and anti-CD18 (Fab/2-leucine zipper fusion with a 6-histidine tag, and anti-CD18 (Fab/2-leucine zipper fusion with a 6-histidine tag, and anti-CD18 (Fab/2-leucine zipper fusion with a 6-histidine tag, and paper fus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel Escherichia coli strain useful for producing polypeptide, deficient in degP and prc encoding protease, and harboring mutant spr gene, product of gene suppresses growth phenotypes of strains harboring prc mutants.
                                                                                                                                                                                                                                                                                                                                                                               Bacterial host, protease, degP, prc, spr, anti-VEGF antibody, antibody, humanised, Apo2 ligand, anti-CD18, anti-tissue factor; 2C4, anti-CD20, anti-vascular endothelial growth factor; anti-Her-2, anti-CD40; Fab; anti-CD111; Fab'; Fab'2, Fab'2-leucine zipper fusion; anti-VEGF Fab.
SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG
                             SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG
                                                                                                                                                                                                                                                                                                                                 Human Apo-2 ligand protein sequence SEQ ID NO:4.
                                                                                                                                                                        ABP51954 standard; protein; 281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Producing a population of activated, Cryptococcus neoformans antigen-
presenting dendritic cells for preventing or treating C. neoformans
infection comprises causing the obtained dendritic cells to present the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to a method of producing a population of activated, Cryptococcus neoformans antigen-presenting dendritic cells, comprising causing the obtained dendritic cells to present the antigen and maturing the dendritic cells. The activated, C. neoformans antigen expressing dendritic cells are useful for treating, or as vaccines or vaccine adjuvants against, C. neoformans infection, or for generating antigen-specific T cells. The present sequence is a human protein shown in the exemplification of the invention
                                                                                                                                         121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
                                                                                                                                                                                                         181 FYYIXSQTYFRFQEEIKENTKADKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY
                                                                                           DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ
                                                                                                                         RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
                             MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
                                                            DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ
                                                                                                                                                                                       FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; fungicide; fungal infection; dendritic cell; antigen;
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Pred. No. 3.8e-137;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cryptococcus neoformans; vaccine; immunostimulant
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Best Local Simi]
Matches 281; (
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Length 281; Indels

Query Match 100.0%; Score 1478; DB 5; Best Local Similarity 100.0%; Pred. No. 3.8e-137; Matches 281; Conservative 0; Mismatches 0;

Sequence 281 AA;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New splice variants of tumor necrosis factor-related apoptosis inducing ligand (TRAIL) isolated from B-lymphocytes and liver, useful to treat diseases or disorders associated with low expression of the variants.
                                                                                                                                                                                                                                                                                          Human; cytostatic; neuroprotective; immunosuppressive; splice variant; tumour necrosis factor; TNF; TNF-related apoptosis inducing ligand; TRAIL; apoptosis; programmed cell death, differentiation; development; cytokine; Apo-2 ligand; Apo-2L; nuclear factor-B; NF-B; type I interferon; tumour; antitumour; gene therapy; cytotxic; cancer; therapeutic; neurodegenerative disease; autoimmune disease; aging;
           1 MAMMEVQGGFSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
                                     DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ
                                                                          RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
                                                                                                               FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY
                                                                                                                         FYYIYSQTYPRFQEIKENTKNDKQMVQYIYKYTSYPDFILLMKSARNSCWSKDAEYGLY
                                                                                                                                                                                                                                                                         Human TNF-related apoptosis inducing ligand (TRAIL) protein.
                                                                                                                                                   SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
                                                                                                                                                             241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG
                                                                                                                                                                                                                                                                                                                                                                                                      "Cytoplasmic domain"

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    note= "Extracellular

                                                                                                                                                                                                                                                                                                                                                                                                                        "Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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/note= "TNF domain"
                                                                                                                                                                                                                  AAU79593 standard; protein; 281 AA.
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/note= "T~
39.
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/note=
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(KHOS/) KHOSRAVI R.
(SAVI/) SAVITZKY K.
                                                                                                                                                                                                                                                                                                                                                   chromosome 3q26.
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                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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The invention discloses isolated, naturally occurring, polypeptide splice variants of human tumourn necrosis factor (TRF)-related apoptosis inducing cligand (TRALL). Apoptosis, or programmed cell death, occurs during normal cellular differentiation and development of multicellular organisms.

Collular differentiation and development of multicellular organisms.

CC (also referred to as Apo-2 ligand, Apo-21). TRALL is a type II membrane protein which induces apoptosis and nuclear factors (NF-B) activation in many tissues and cells. Receptors for TRALL include two death domain.

CC containing receptors. DR4 and DR5, as well as two decoy receptors, DCR1 and DR2, lacking the interferons, induces apoptosis in tumour cells, whereas normal cells are relatively resistant without showing significant toxic and beR2, lacking the interferons, induces apoptosis in tumour cells, whereas normal cells are relatively resistant without showing significant toxic and titumour agent. The naturally occurring splice variants may differ in their cellular distribution, expression levels/timing and activity.

CC antitumour agent. The naturally occurring splice variant polyapeptides and polynucleotides can be used in gene therapy, to raise antibodies, to determining these factors could provide possible mechanisms for the confirming these factors could provide possible mechanisms for the antipodice of the splice variant TRALL products and modulate its activity (agonists which bind the variant TRALL products and modulate its activity (agonists and antagonists). Pharmaceutical compositions, comprising an expression vector or any of the antino acid sequences. The artibodies may also have a therapeutic thin amino acid sequences. The antibodies may also have a therapeutic utility in blocking or decreasing the activity of thesess, also and all organisms and products. Diseases that may be treated in clude cacer, neurodegenerative diseases, autoimmune diseases, diseases involved in the non-normal conducting ligand (TRALL) protein the wild-type in 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1478; DB 5;
Pred. No. 3.8e-137;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 100.
Matches 281; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181
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120

DDSYMDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ

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Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis; multiple sclerosis, retrinitis pigmentosa; cerebellar degeneration; aplastic anaemia; myocardial infarction; stroke; reperfusion injury; toxin-induced liver disease; cancer; lupus; herpes virus infection.
                                                                                                                                                                                                                                                                 Novel isolated Apo-3 polypeptide useful for inducing apoptosis in mammalian cells, for generating antibodies, in affinity purification techniques, and in competitive-type receptor binding assays.
                                                                              "Transmembrane domain"
                                                                                               /note= "Extracellular domain"
                                                                                                                /note= "N-glycosylated"
                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                     Example 4; Fig 4; 52pp; English.
                                                                                                                                                                                    96US-0026943P.
                                                                                                                                                                   97US-00928069
                                                                                      .281
                                                                       15. .40
/note= "'
                                                                                                                                                                                                     (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                        WPI; 2003-173840/17.
N-PSDB; ABX15469.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 281 AA;
                                                                                                      Modified-site
                                                                                                                                                                                                                        Ashkenazi AJ;
                                                                                                                                                                                    23-SEP-1996;
                                            sapiens
                                                                                                                                 US6462176-B1
                                                                                                                                                                   11-SEP-1997;
                                                                                                                                                  08-OCT-2002.
                                                                    Domain
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The invention relates to an Apo-3 polypeptide having an extracellular domain (BCD) sequence and a death domain sequence. The Apo-3 polypeptide has been found to stimulate or induce apoptotic activity in mammalian cells. Human Apo-3 exhibites similarities to the tumour necrosis factor receptor (TNFR) family of polypeptides. The invention also relates to a chineric molecule comprising an extracellular domain sequence comprising residues 1-198 of Apo-3 fused to a heterologous amino acid sequence. The Apo-3 polypeptide is useful therapeutically to induce apoptosis in mammalian cells. Decreased levels of apoptosis has been associated with conditions such as cancer, lupus, and herpes virus infection. Increased levels of apoptosis are associated with disease such as acquired conditions such as cancer, lupus, and herpes virus infection. Increased levels of apoptosis are associated with disease such as acquired immunodeficiency syndrome (AIDS), Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis, multiple sclerosis, retinitis pigmentosa, cerebellar degeneration, aplastic anaemia, myocardial infarction, stroke, reperfusion injury, and toxin-induced liver disease. The Apo-3 polypeptide is also useful in non-therapeutic applications such as in quantitative diagnostic assays for Apo-3, in affinity purification containing unknown quantities of Apo-3 may be prepared, in generating antibodies, as standards in assays for Apo-3, in affinity purification techniques, and in competitive-type receptor binding assays. The chimeric molecule is useful therapeutically to inhibit apoptosis or nuclear factor. App-3 antibodies. The present sequence represents polypeptide sequence of the human Apo-2 ligand protein which is also reported to be involved in the Apo-2 intaid death. In the current invas massays in which is appopted to be involved in the Apo-2 ligand protein which is abore to be involved in the Apo-2 in a death of the appopunce of the human Apo-2 ligand protein which in whe competitive to be involved in the Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the Apo-2 ligand protein was measured on human lymphoid cells
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Query Match 100.0%; Score 1478; DB 6; Best Local Similarity 100.0%; Pred. No. 3.8e-137; Matches 281; Conservative 0; Mismatches 0;
                                             Sequence 281 AA;
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Length 281;
                            Indels
100.0%; Score 1478; DB 6; 100.0%; Pred. No. 3.8e-137;
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                            0; Mismatches
                            281, Conservative
            Local Similarity
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Query Match

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Gaps

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Length 281; Indels

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                                                                                         181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLLMKSARNSCWSKDAEYGLY 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated Apo-3 polypeptide. The Apo-3 polypeptides are useful for stimulating or inducing apoptotic activity in mammalian cells e.g. cancer cells, or for in vivo or ex vivo gene therapy techniques. The Apo-3 chimeric molecules are useful for inhibiting apoptosis, or as immunogens used in generating antibodies. The antibodies may be used to block excessive apoptosis, for instance in neurodegenerative disease, or to block potential autoimmune/ inflammatory effects of Apo-3 resulting from NP-kappaB activation. The uncleic acid sequences are useful as diagnostics for tissue-specific typing, for preparing Apo-3 polypeptides, or for generating transgenic or knockout animals. The transgenic or knockout animals are useful in
                                180
RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated Apo-3 polypeptides, useful for stimulating or inducing apoptotic activity in mammalian cells, e.g. cancer cells, or for in vivo or ex vivo gene therapy techniques.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         present
                       RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
                                                                  PYYIYSQTYPRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY
                                                                                                                                                                                                                                                                                                                                                                                               Human, Apo-2 ligand, apoptosis, gene therapy; inflammation, cancer; neurodegenerative disease; immunosuppresive; tissue typing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         developing and screening of therapeutically useful reagents. The pequence represents the amino acid sequence of human Apo-2 ligand
                                                                                                                                     SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
                                                                                                                                                       241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG
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                                                                                                                                                                                                                                                          ABU10205 standard; protein; 281
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97US-00928069.
                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                              ligand;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-438872/41.
                                                                                                                                                                                                                                                                                                                                                              Human Apo-2 ligand.
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Novel isolated PRO polypeptides e.g. PRO240, PRO381, PRO540, useful for treating tumor, preferably cancer, or for treating neuronal, glial,
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, Wood WI;
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Watanabe CK,
                   99WS-0116533P.
99WO-US005028.
99US-0123618P.
99US-0128615.
99US-0131294P.
99WO-US012252.
                                                                                        9903-0140650P
9903-0141037P
9903-0141037P
9903-00380137
9900-00380138
9900-00302011
9903-00380913
9903-0043297
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99WO-US028313.
99WO-US028634.
99WO-US028551.
99WO-US0300095.
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2000WO-US003565.
2000WO-US004341.
2000WO-US004342.
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2001US-00872034.
2001US-00872035.
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2000WO-US022031.
2000WO-US023522.
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2000US-0187202P.
2000WO-US006884.
99US-0115554P
99US-0115558P
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2000WO-US013705
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2001US-00882636
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2001US-00918585.
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2001US-00866034
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GETH ) GENENTECH INC
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N-PSDB; ACA58016.
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18-FEB-2000;
02-MAR-2000;
03-MAR-2000;
15-MAR-2000;
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17-MAY-2000;
22-MAY-2000;
12-JAN-1999;
12-JAN-1999;
02-JAN-1999;
08-MAR-1999;
10-MAR-1999;
12-APR-1999;
27-APR-1999;
02-JUN-1999;
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23-AUG-2000;
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Shelton DL,
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02-DEC-1999
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                                                 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
                                                              DDSYMDPIDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
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                                                                                                                                                                                                                                                                                                                          Human; tumour; cancer; neoplasia; liver cancer; sarcoma; breast cancer; ovarian cancer; renal cancer; colorectal cancer; melanoma; uterine cancer; prostate cancer; lung cancer; bladder cancer; leukaemia; gastric cancer; pancreatic cancer; vulval cancer; thyroid cancer; central nervous system cancer; hepatic carcinoma; glioblastoma; neuronal disorder; glial disorder; astrocytal disorder; hypothalamic disorder; glandular disorder; macrophagal disorder; epithelial disorder; stromal disorder; inflammatory disorder; angiogenic disorder; immunologic disorder.
                     MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGJACFLKE
                                                                                         RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
                                                                                                      RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
                                                                                                                                 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY
         MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
                                                                                                                                           SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
                                                                                                                                                                         SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
                                                                                                                                                                                                                                                                                                         Human neoplasia inhibiting PRO polypeptide PRO1096.
                                                                                                                                                                                                                                               ABU71443 standard; protein; 281 AA
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98US-0079920P
98US-0081545P
98US-0081545P
98US-008160P
98US-008160P
98US-0096891P
98US-0096891P
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98US-0096891P
98US-0096894P
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98US-0112420P.
98US-00218517.
98US-0113296P.
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24-APR-1998;
29-APR-1998;
12-MAY-1998;
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17-AUG-1998;
17-AUG-1998;
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22-DEC-1998;
05-JAN-1999;
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14-SEP-1998
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The invention relates to an isolated secreted and transmembrane polypeptide, designated as PRO polypeptide, PRO polypeptide lacking its associated signal peptide or PRO polypeptide can antibody without its associated signal peptide. The PRO polypeptide or an antibody binding to it is useful for inhibiting the growth of a tumor cell. A composition containing a PRO polypeptide is useful for inhibiting neoplastic cell growth or for treating a tumour, preferably cancer (such as liver, breast, ovarian, renal, colorectal, uterine, prostate, lung, bladder, gastric, pancreatic, vulval, thyroid, central nervous system cancer, hepatic carcinomas, sarcomas, qlioblastomas, melanoma or leukaemia) in a mammal. The PRO polypeptide is useful for identifying its agonists. The PRO polypeptide or an antibody binding to it is useful in the preparation of a medicament for treating a condition which is responsive to the PRO polypeptide or an antibody binding to it. The PRO polypeptide or an antibody binding to it is also useful for treating curveronal, glial, astrowal, blastocolic, inflammatory, angiogenic and immunologic disorders. The present sequence represents the amino acid sequence of a PRO polypeptide of the invention
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hypothalamic, stromal, inflammatory, angiogenic and immunologic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 1478; DB 6; Length 281; 100.0%; Pred. No. 3.8e-137; ive 0; Mismatches 0; Indels 0
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tumour necrosis factor-related apoptosis inducing ligand,
atopic skin inflammation.
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                                                       Claim 32; Fig 54; 186pp; English
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Matches 281; Conservative
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comprises measuring the expression level of tumour necrosis factor (TNF) - related apoptosis inducing ligand (TRAIL) gene in a specimen from the patient and comparing this level with the level in healthy persons. TRAIL gene expression is decreased in patients. The nucleic acids and polypeptide can be used to screen for agents for the treatment of allergic diseases, possibly using a transgenic rodent as a model animal for the disease, with effectiveness determined by changes in expression levels or protein activity. The method is useful for the diagnosis, examination, prevention and treatment of allergic diseases, including atopic skin inflammation. The sequence presented is the human TRAIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hyperproliferative disorder; Theumatoid arthritis; Parkinson's disease; hyperproliferative disorder; Alzheimer's disease; Hashimoto's disease; neurodegenerative disorder; Alzheimer's disease; Hashimoto's disease; mallergic disorder; acquired immune deficiency syndrome; ocular disorder; myasthenia gravis; autoimmune decertar; Huntington's disease; vaccine; septic shock; multiple sclerosis; inflammatory disorder; liver injury;
                                                                                                                                                                                                                                                                                                                                The invention discloses a method for examining allergic diseases, which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; TNF-related apoptosis-inducing ligand; Kaposi's sarcoma; cancer;
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                                                                                                                                                                                                            Measurement of the expression level of TNF related apoptosis inducing ligand gene for diagnosis and examination of allergic disease and screening agents for allergic disease treatment.
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                                                                                                              Tsujimoto G;
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100.0%; Pred. No. 3.8e-137;
live 0; Mismatches 0;
                                                                                                              Gunji S,
                                                                                                                                                                                                                                                                                           Disclosure, Page 51-52; 58pp; Japanese.
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                                                                                                              Kagaya S,
                                                                           JAPAN GEN AGENCY NATION
                  06-APR-2001; 2001JP-00108631.
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Best Local Similarity 100.
Matches 281; Conservative
                                                       GENOX RES INC
                                                                                                              Sugita Y, Heishi M,
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                                                                                                                                                  2003-093037/08.
                                                                                                                                                                         N-PSDB; ABX13715
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Antibodies of the invention are also useful for treating cardiovascular disorders, carebrovascular disorders, thrombotic microangiopathies, and ulcerative colitis and for wound healing. The invention is also used the new accines. The present sequence is human TRAIL protein also
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel antibody against TNF-related apoptosis inducing ligand, useful for preventing, treating and ameliorating cancers and other hyperproliferative disorders, binds immunospecifically to TRAIL receptor
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infectious diseases; myelodysplastic syndrome; cardiovascular disorder; graft-versus-host disease; toxin-induced liver disease; cachexia; AIDS; cerebrovascular disorder; thrombotic microangiopathy; aplastic anaemia; ischaemic injury; anorexia; diabetes; ulcerative colitis; psoriasis; asthma; AIDS; therapy; TRAIL receptor; TRAIL-R; AIM-I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         invention relates to antibodies that immunospecifically bind to
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Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                  Rosen CA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 2; Page 392-393; 405pp; English
                                                                                                                                                                                                                                                                                                                                                                                                  Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Sco
100.0%; Pre
tive 0; N
                                                                                                                                                                                                                                                                              2001US-0331309P.
                                                                                                                                                                                                                                       13-NOV-2002; 2002WO-US036431
                                                                                                                                                                                                                                                                                                                        15-AUG-2002; 2002US-0403376P.
                                                                                                                                                                                                                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC.
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1es 281; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                  Salcedo T, Roschke V,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 281 AA;
                                                                                                                                                          WO2003042367-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polypeptide.
                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                            14-NOV-2001;
07-MAY-2002;
                                                                                                                                                                                                  22-MAY-2003
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276. .281
/note= "C-terminal fragment specifically claimed in claim
26"
181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDFILLMKSARNSCWSKDAEYGLY 240

    124
    note= "N-terminal fragment specifically claimed in claim

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an antibody that specifically binds: (a) the human tumor necrosis factor (TNP) related apoptosis inducing ligand (TRAIL) protein appearing as ABU08558; (b) a soluble human TRAIL polypeptide; (c) a polypeptide comprising amino acids 124-276 of ABU08558, or (d) a fragment of the TRAIL protein. Also included is an antigen-binding fragment of the antibody (a monoclonal antibody), a hybridoma cell line that produces the antibody. The antibody), a assays to detect the presence of TRAIL polypeptides, either in vitro or in vivo, purifying TRAIL by affinity chromatography, blocking binding of TRAIL to target cells and thus inhibiting a biological activity of TRAIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124. .276
/note= "This region is specifically claimed in claim 20"
276. .281
                                                                                                                                                                                                                                                                                              tumour necrosis factor; apoptosis; haemostatic; immunosuppressive; antiinflammatory; dermatological; thrombotic microangiopathy; thrombotic thrombotytopaenic purpura; TTP; HUS; SLB; clotting disorder; adult haemolytic uraemic syndrome; cardiac problem; paediatric AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antibody which binds to human tumor necrosis factor related sis inducing ligand protein, useful for inhibiting TRAIL-mediated sis of a target cell, or blocking binding of TRAIL to a target
                                                                                                                                                                                                                                                                              Human; TNF related apoptosis inducing ligand; TRAIL;
                                                 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG
                                SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG
                                                                                                                                                                                                                                                Human TNF Related Apoptosis Inducing Ligand, TRAIL.
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                                                                                                                                              ABU08558 standard; protein; 281
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95US-00548368.
95US-00670354.
98US-00048641.
98US-00190046.
                                                                                                                                                                                                                                                                                                                                                                 systemic lupus erythematosus.
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                                                                                                                                                                                                               (first entry)
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N-PSDB; ABX93869.
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26-MAR-1998;
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                                                                                                                                                                              ABU08558;
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us-10-662-431-2.rag

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The antibody is useful for treating disorders mediated or exacerbated by TRAIL, e.g. thrombotic microangiopathies, e.g. thrombotic thrombotycypaenic purpura (TTP), adult haemolytic uraemic syndrome (HUS) (even though it can strike children as well) small blood vessel clotting disorders e.g., cardiac problems in paediatric AIDS patients and systemic lupus erythematosus (SLE). The present sequence represents human TRAIL
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                                                                                                                                                                                                                                                                 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
                                                                                                                                                                                                                                                                                                                           RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
                                                                                                                                                                                                                                                                                              DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is the protein sequence of human TRAIL polypeptide. The invention relates to compositions comprising heterotrimeric complexes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New heteromultimeric complex having a first polypeptide member of the tumor necrosis factor (TNF) ligand family, and a second different member of TNF ligand family, useful for treating cancer, osteoporosis or an
                                                                                                                                                                                                                       MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
                                                                                                                                                                                                                                                                                                                                                                                          FYYIYSQTYFREQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY
                                                                                                                                                                                                                                                                                                                                                                                                           FYXIXSQIYFRFQEEIKENTKNDKQMVQYIYKYTSYPDFILLMKSARNSCWSKDAEYGLY
                                                                                                                                                                                                    MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
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                                                                                                                                        Length 281;
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immunomodulator; osteopathic.
                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 1478; DB 6; 100.0%; Pred. No. 3.8e-137;
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                                                                                                                                                                     0; Mismatches
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                                                                                                                                                                         Conservative
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                                                                                                                                                        Best Local Similarity
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                                                                                                           Sequence 281 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO2003040307-A2
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                                                                                                                                                                     281;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
            the detection, prevention and treatment of disease. In one embodiment, the heterotrimeric comprises full-length or extracellular portions of TRAIL and full-length or extracellular portions of TRAIL and full-length or extracellular portions of other TNF ligand family members, preferably RANKL. The heterotrimeric complexes of the invention are useful for treating an autoimmune disease, cancer or osteoporosis, and particularly for inhibiting cancer cell proliferation, increasing B cell proliferation, or inducing apoptosis of T cells. A claimed method of inducing apoptosis of T cells and retrotrimeric complex consisting of Faal and LIGHT, TNF-alpha. Inmphotoxin-beta or TRAIL. A claimed method of inhibiting cancer cell proliferation involves administering a heterotrimeric complex consisting of comprises administering an antibody against a complex comprising RANKL and TRAIL.
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tumour necrosis factor (TNF) ligand family members, and their use in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; TRAIL receptor; tumour necrosis factor; TNF;
                                                                                                                                                                                                                                                                                                                                                              Natch 100.0%; Score 1478; DB 6; Local Similarity 100.0%; Pred. No. 3.8e-137; Nes 281; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human TRAIL receptor-associated protein.
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                                                                                                                                                                                                                                                                                                                            Sequence 281 AA;
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The invention relates to an isolated antibody comprising a first amino acid sequence having 95 % identity to a second amino acid sequence of acid sequence having 95 % identity to a second amino acid sequence of either variable heavy chain or light chain-complementarity determining regions (WHCDR1)/VLCDR1, WHCDR2/VLCDR2 or WHCDR3/VLCDR3 appearing as ABG71996-ABG71911 being specific for human TRAIL receptors 1-4 (TMF (Tumour necrosis factor) related apoptosis-inducing ligand receptor, also known as TR4, TR5, TR7 and TR10). Also included are an isolated cell that produces the antibody, an antibody that binds the same epitope on a TR4 polypeptide or detecting, diagnosing, prognosing or and other hyperproliferative disorders) using the antibodies, a cancers, and other hyperproliferative disorders) using the antibodies, a cancer of whyridoma cell line selected from the hybridoma cell lines contained in hybridoma cell lines antibodies expressed by these cancers and pra-1313 and the antibodies expressed by these cancers and pra-1313 and the antibodies expressed or decreased apoptosis, e.g. cancer (such as colon, prease, useful for diagnosing or treating a disease or disorder associated with increased decreased apoptosis, e.g. cancer (such as colon, prease, useful for spanceatic, lung, gastrointestinal, and Kaposi's sarroma), graft-versus-color disease (WHD), infectious disease, acquired immunodeficiency syndrome (AIDS), or neurodegenerative disorders (e.g. Alzheimer's disease, about as theumatosid arthritis, and pooriasis, cardiovascular disorders, in promoting angiogenesis, wound healing, and in regulating immune response. Comprody is administered in combination with a chemotherapeutic agent as the body is administered in combination with a chemotherapeutic agent carbibody is useful as a diagnosic tool to monitor the expression of antibody is useful as a diagnosic tool to monitor the expression of a human TRALL receptor expression on cells, to detect, purify, and target the colory and in immunosasy's for qualitatively
                                                                                                                                                                                                                                                                            comprises
                                                                                                                                                                                                                                                                        Novel antibody for treating, or preventing disease or disorder, compriamino acid sequence having identity to other amino acid sequence of either variable heavy/light chain-complementarity determining regions.
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100.0%; Pred. No. 3.8e-137
ive 0; Mismatches 0;
                                                                                                                                                                                   Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 366; 375pp; English
                                                                                                                                                                                Ruben SM,
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08-NOV-2000; 2000US-0246612P.
16-NOV-2000; 2000US-024847P.
27-NOV-2000; 2000US-025294P.
04-JUN-2001; 2001US-0295018P.
                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC.
                                                                                         2001US-0327359P
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                               1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNBLKQMQDKYSKSGIACFLKE
                                                                                               DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ
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                                                    SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG
                                  SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG
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GVHD; dermatological; immunosuppressive; antinflammatory; antirheumatic; antiarthritic; cytostatic; antianaemic; antiallergic; antiasthmatic; neuroprotective; ophthalmological; tuberculostatic; anti-HIV; antiarteriosclerotic; vasotropic; thyromimetic; haemostatic; cancer; autoimmune disease; graft versus host disease; gVHD; inflammatory disorder; proliferative disorder; single chain antibody; antibody; human; TRAIL; tumour necrosis factor. APRIL; scFv; immunospecific; tumour necrosis factor delta; TNF-delta; Human tumour necrosis factor TRAIL. Z ABP60546 standard; protein; 281 28-MAR-2003 (first entry) WO200294192-A2. Homo sapiens. 28-NOV-2002 ABP60546; 음

22-MAY-2002; 2002WO-US016106.

24-MAY-2001; 2001US-0293100P.

(HUMA-) HUMAN GENOME SCI INC.

Ruben SM;

WPI; 2003-156740/15.

Novel isolated antibody that immunospecifically binds tumor necrosis factor delta, useful for treating, preventing or ameliorating Non-Hodgkin's lymphoma, multiple myeloma, rheumatoid arthritis or Sjogren's syndrome.

Disclosure; Page 216-217; 225pp; English.

The invention relates to a novel antibody or its fragment, which immunospecifically binds tumour necrosis factor Delta (TNF-delta/APRIL). The antibody of the invention has dermaclogical, immunosuppressive, antialtergic, antiathritic, cytostatic, antianaemic, antialtarthritic, cytostatic, antianaemic, antialtarthritic, cytostatic, antianaemic, cutialtarthritic, antibosoriatic, antianaemic, antialtarthritic, cytostatic, antianaemic, antialtarthritic, cytostatic, antianaemic, antialtarthritic, antibosoriatic, antianaemic, antialtarthritic, antibosoriatic, antianaemic, antianaemic, antianaemic, antianaemic, antianaemic, antianaemic, antianaemic, antianaemic, antianathritic, antibosoriatic, and haemostatic activity.

The antibody or its fragment are useful for treating, preventing or ameliorating cancer such as Non-Hodgkin's lymphoma or multiple myeloma in host disease (GVHD). The autoinmune disease is systemic lupus cythematosus, rheumatoid arthritis or Sjogrem's systemic lupus cytheatesus, rheumatoid arthritis or Sjogrem's systemic lupus cytheatesus or disorder associated with aberrant APRIL or ARRIL receptor expression or aberrant function of APRIL or ARRIL receptor expression or aberrant function of APRIL or ARRIL receptor as autoimmune neutropenia, haemolytic anaemia, dermaritis, cuberculosis, diaberes mellitus, psoriasis, cancer of the immune system, particularly B cell cancers, immune disorders such as myasthenia gravis, Hashimoto's disease, immunodeficiency syndrome (AIDS)), and infectume necrosis factor TRAIL

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Gaps

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Length 281;

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TRAIL receptor; TR4; cancer; Kaposi's sarcoma; cerebellar degeneration; hyperproliferative disorder; neurodegenerative disorder; immune disorder; Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis; retinitis pigmentosa; Huntingon's disease; amyotrophic lateral sclerosis; rheumatoid arthritis; multiple sclerosis; Sjogran's syndrome; asthma; bilary cirrhosis; Behcet's disease; Sjogran's syndrome; asthma; bilary cirrhosis; Behcet's disease; Crohn's disease; allergic disorder; glomerulonephritis; immune deficiency syndrome; myasthenia gravis; polymyositis; inflammatory disorder; rheumatoid arthritis; septic shock; infectious disease; acquired immunodeficiency syndrome; viral infection; infcretuous disoase; acquired immunodeficiency syndrome; oracher; anorexis; stroke; cardiovascular disorder; myelodysplastic syndrome; achexia; anorexis; stroke; cardiovascular disorder; peripheral artery disease; limb ischaemia; arrhythmia; congestive heart failure; neovascularisation; ocular disorder; wound healing; angiogenesis; transplantation; human.
                                                                                                                                                                                DDSYWDPNDEESMINSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
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                                100.0%; Score 1478; DB 6;
100.0%; Pred. No. 3.8e-137;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human TR4 ligand, TRAIL protein.
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04-JUN-2001; 2001US-0294981P.
21-SEP-2001; 2001US-0323807P.
09-OCT-2001; 2001US-0323847P.
07-NOV-2001; 2001US-0331310P.
20-DEC-2001; 2001US-0341237P.
05-APR-2002; 2002US-0369860P.
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                                                   Best Local Similarity 100.
Matches 281, Conservative
Sequence 281 AA;
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                                  Query Match
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treating, preventing or ameliorating cancer (e.g. colon, breast, uterine, present line present line present line present line present line presents the preventing or ameliorating cancer (e.g. colon, breast, uterine, pancreatic, lung, gastrointestinal or central nervous system cancer e.g. medulloblastoma, neuroblastoma, glioblastoma and Kaposi's sarcoma) in human. They are useful for detecting expression of TR4 polypeptide and detecting disposing, prognosing or monitoring cancers and other hyperproliferative disorders. Antibodies of the invention are useful for treating, preventing neurodegenerative disorders (e.g. Alzheimer's disease, arkinoor's disease, amyotrophic lateral sclerosis, retinitis pigmentosa, cerebellar degeneration and Huntington's disease, cerebellar degeneration and Huntington's disease, cerebilar degeneration and Huntington's disease, cerebilar degeneration and Huntington's disease, commune disorders (e.g. lupus, rheumatorid arthritis, mustabhenia gravis, immune-related glomerulonephritis, mustabhenia gravis, collymyositis, immune-related glomerulonephritis, myandrome (Algorders (e.g. asthma, allergic disorders and rheumatoid arthritis), chapters (e.g. asthma, allergic disorders and rheumatoid arthritis), cherpes viral infections and other viral infections) and proliferative disorders. They are also useful for treating cardiovascular disorders including peripheral concexia and toxin-induced liver diseases (such as alcohol). They are also useful for treating cardiovascular disorders including peripheral cancerial infertion and ocular disorders, for wound healing, for with neovascularisation and ocular disorders, for wound healing, for treating and as adjuvants to enhance immune responsiveness to specific antigeness and as adjuvants to enhance in wunner and protein therapy and transplantation or recovery from surgery, trauma, radiation therapy and transplantation are sequence is human TR4 ligand, TRAIL protein in the invention invention relates to novel antibodies that immunospecifically Novel antibody useful for treating cancers and other hyperproliferative disorders, immunospecifically binds to TRAIL receptor and comprises variable heavy or light chain complementarity determining regions. Vaughan TJ; Dobson CL, Rosen CA, Albert VR, Disclosure; Page 300-301; 301pp; English. Ruben SM, used in the invention present Salcedo T,

Sequence 281 AA;

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                                                                                                          1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
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       ; Score 1478; DB 6;
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0; Mismatches 0;
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AAO31151 standard; protein; 281 RESULT 34 AAO31151 ID AAO3 XX

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The invention relates to a combination comprising CDNAs which are expressed in a disorder or process associated with DNA methylation. The combination and cDNAs are useful for diagnosing, staging, treating or monitoring treatment of cancer, e.g. colon cancer and for detecting changes in expression of genes encoding proteins that are associated with DNA methylation. The protein is useful for screening molecules or compounds to identify at least one ligand that binds to the protein and for producing an antibody. The present sequence represents the amino acid sequence of a protein expressed in a disorder or process associated with
DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
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                                                                                                               PYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human TNF-related apoptosis inducing ligand TRAIL Incyte 059509CD1.
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100.0%; Pred. No. 3.8e-137;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 56-57; 66pp; English.
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Matches 281; Conservative
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(JONE/) JONES D A.
(KARP/) KARPF A R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated antibody or its fragments such as VHCDR1 (heavy chain variable domain complementarity determining region), VHCDR2, VHCDR3, VLCDR1 (light chain variable domain complementarity determining region), VLCDR2 (Light chain variable domain complementarity determining region), VLCDR2 or VLCDR3. The antibody or its fragment immorsopecifically binds TRAIL (tumour necrosis factor; TNR-related repoptosis-inducing ligand) receptor 7 (TR7). TR7 is also referred to as TRAIL receptor 2 (TRAIL. FC), death receptor 5 (DR5) and KILLER. The antibody or its fragment is useful for treating, preventing or ameliorating a cancer, e.g. colon, breast, uterine, pancreatic, lung or gastrointestinal cancer or Kaposi's sarcoma or cancer of the central nervous system such as medulloblastoma, neuroblastoma or glioblastoma or graft versus host disease, AIDS (acquired immune deficiency syndrome) or a neurodegenerative disorder. The invention is useful in antibody
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                                                                                                                                   Human; protein coordinate data; heavy chain variable domain; VH; cancer; complementarity determining region; CDR; light chain variable domain; VL; TRAIL receptor 7; TR7; tumour necrosis factor; KILLER; death receptor 5; DR5; TRAIL receptor 2; TRAIL-R2; TNF-related apoptosis-inducing ligand; Kaposi's sarcoma; central nervous system; medulloblastoma; neuroblastoma; glioblastoma; graft versus host disease; antibody therapy; nootropic; AlDS; acquired immune deficiency syndrome; neurodegenerative disorder; immunosuppressive; neuroprotective; antibody therapy; antibody.
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                                                                                          Human TNF-related apoptosis-inducing ligand (TRAIL)
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100.0%; Pred. No. 3.8e-137;
ive 0; Mismatches 0;
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2002US-0403370P.
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                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-569250/53.
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                                                                                                                                                                                                                                                                                                                                                                                             WO2003054216-A2
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                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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15-AUG-2002;
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  AA031151;
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N-PSDB; ADC35201.
                                                                                                   Sequence 281 AA;
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                                                                          the invention.
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Best Local 8
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          RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
                         RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
                                                            240
                                                                                    240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel isolated Apo-2 ligand variant polypeptide useful for treating cancer or an immune-related disease such as multiple sclerosis, comprises amino acid substitutions in the native sequence of the Apo-2 ligand.
                                                                                                                                                                                                                                                                                                    Apo-2 ligand, DRS.Apo2L complex, receptor contact region, high solvent accessibility; cytostatic; antiarthritic, neuroprotective; trimer, apoptosis; DR4 receptor; DR5 receptor; colon; colorectal cancer; lung; breast; immune-related disease; arthritis; multiple sclerosis;
                                                                           FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY
                                                                                                                            SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
                                                                                                             SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG
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                                                                                                                                                                                                                                                                            Native human Apo-2 ligand protein.
                                                                                                                                                                                                   ADB61471 standard; protein; 281
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                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GETH ) GENENTECH INC
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N-PSDB; ADB61470.
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                                                                                                                                                                                                                                                                                                                                           lung; breast;
native; human
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the Apo-2 ligand composition or the Apo-2 ligand trimer is useful for treating cancer (such as lung, breast, colon or colorectal cancer) or an immune-related disease (such as arthritis or multiple sclerosis) in a mammal, by administering to the ammal an effective amount of the Apo-2 ligand variant polypeptide, Apo-2 ligand composition or Apo-2 ligand trimer. This sequence represents the native human Apo-2 ligand protein of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DDSYMDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
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                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human; tumour necrosis factor; TNF ligand; endokine alpha;
excessive bone resorption disorder; osteoporosis; Paget's disease;
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                                                                                                                                                                                                                                                                                       Length 281;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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                                                                                                                                                                                                                                                                                          Score 1478; DB 7;
Pred. No. 3.8e-137;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                    100.0%;
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30-OCT-2001; 2001US-0330761P.
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                                                                                                                                                                                                                                                                                                                                                  Matches 281; Conservative
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                                                                                                                                                                                                                                                                                                                    Similarity
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                                                           tumour necrosis factor family ligand. A composition comprising the isolated antibody or its fragment is used for treating an individual in need of decreased level of endokine alpha activity. The endokine alpha polypeptide present in a heterotrimeric complex is used for treating an individual having a disorder associated with excessive bone resorption, e.g. osteoporosis, Paget's disease or arterial calcification. Treating an individual having a disorder associated with insufficient bone resorption comprises administering an endokine alpha antagonist, which is the antibody that binds specifically to endokine alpha polypeptide. The present sequence represents the amino acid sequence of a tumour necrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FYYISQTYFRFQEBIKENTKNDKQMVQYIYKYTSYPDFILLMKSARNSCWSKDAEYGLY
                                              The invention relates to an isolated nucleic acid molecule encoding a
                                                                                                                                                                                                                                                                                                                                                            1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
                                                                                                                                                                                                                                                                                                                                                                                                                              DDSYMDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         predictor set; protein tyrosine kinase activity modulator; protein tyrosine kinase; cytostatic; gene therapy; drug sensitivity; genetic profile; cancer; human.
                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                            100.0%; Score 1478; DB 7;
100.0%; Pred. No. 3.8e-137;
ive 0; Mismatches 0;
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           Disclosure; SEQ ID NO 20; 145pp; English
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                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                               factor family ligand
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                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                            Sequence 281 AA;
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                                                                                                                                                                                                                                                                                                                         281,
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                                                                                                                                                                                                                                                                                                                                                                                                                            61
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the response to cerial to treatment with a compound title included the control of pathway. Also described: (1) predicting whether a compound is capable of modulating the activity of cells, comprising obtaining a sample of cells, determining whether the cells express a plurality of markers, and determining whether the cells express a plurality of markers, and correlating the expression of the markers to the compound's ability to correlate the activity of the cells; (2) a plurality of cell lines for identifying polymucleotides and polypeptides whose expression levels correlate with compound sensitivity or resistance of cells associated with a disease state, and (3) identifying polymucleotides and colls correlated with a disease state, compound sensitivity or resistance of cells associated with a disease state, and subjecting the plurality of associated with a disease state, compounds sensitivity or resistance of cells compounds that predict the sensitivity or cell since to polymucleotides or polypeptides that predict the sensitivity or cells associated with a disease state by using the expression pattern of the microarray of polymucleotides and collymucleotides and polypeptides are useful in predicting the carrivity of compounds that interact with protein tyrosine kinase pathways. These may be used in determining drug concern tyrosine kinase pathways. These may be used in determining drug sensitivity in patients to allow the development of individualized cancern based on patient response at a molecular level. The present concern based on patient response at a molecular level. The present concern based on patient response at a molecular level. The present
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                                                                                                                                                              The present invention describes a predictor set comprising a plurality of polynucleotides or polypeptides whose expression pattern is predictive of the response of cells to treatment with a compound that modulates protein
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                      polynucleotides and polypeptides for predicting the activity of sounds that interact with protein tyrosine kinases and/or protein
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                                                                                                               ID NO 269; 139pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADD19010 standard; protein; 281
                                                                     tyrosine kinase pathways.
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Query Match
100.0%; Score 1478; Sest Local Similarity 100.0%; Pred. No. 3.8 Matches 281; Conservative 0; Mismatches
                                                                                                  HID STANDARD STANDARD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention relates to novel human genes and gene product which are implicated in certain disease states. Compounds which modulate the proteins of the invention may have cytostatic, antiinfilammatory. Ophthalmological, antiateriosclerotic or vulnerary activities. The sequences of the invention may be useful for gene therapy. The invention may be useful for gene therapy. The invention may be useful for gene therapy. The invention may be useful for diagnosing or treating a hypoxia-regulated condition, erthropoiesis, andiogenesis, apoptosis, inflammation, erythropoiesis or the biological response to hypoxia conditions including processes such as glycolysis, glucomeogenesis, glucome synthesis. The disease such as glycolysis, iron transport or nitric oxide synthesis. The disease includes cancer, ischaemic conditions, reperfusion injury, retinopathy, neonatal stress, pre-eclampsia, atherosclerosis, a disease related protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New substantially purified polypeptide, useful for diagnosing or treating a hypoxial aregulated condition, such as cancer, ischemia, reperfusion injury, retinopathy, pre-eclampsia, atherosclerosis, inflammation, or wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    240
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                      hypoxia-regulated condition; tumourigenesis; angiogenesis; apoptosis; inflammation; erythropoiesis; glycolysis; gluconeogenesis; glucose transportation; catecholamine synthesis; iron transport; nitric oxide synthesis; cancer; lachaemic condition; reperfusion injury; retinopathy; neonatal stress; pre-eclampsia; atherosclerosis; inflammatory condition; wound healing.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Harris RA, Naylor S, Mundy CR;
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antiarteriosclerotic; vulnerary; gene therapy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ward NR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (OXFO-) OXFORD BIOMEDICA UK LTD
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05-OCT-2001; 2001GB-00024037.
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des 281; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               White J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-290046/28.
N-PSDB; ADD19011.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kingsman SM,
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The invention relates to methods and compositions for treating or ameliorating a disease or disorder of the gastrointestinal tract. The method involves administering a composition comprising tumour necrosis factor (TNF)-gamma-beta and its receptors DR3 and TR6 to a person with, or suspected of having the disease or disorder. The antagonist of TNF-amma-beta is useful for treating or ameliorating a gastrointestinal tract disease or disorder, specifically an inflammatory bowel disease, e.g. Crohn's disease or ulcerative colitis. The present sequence is human TRAIL protein. This sequence is used to illustrate the method of the
                                                                                                                                                                                                   Gastrointestinal tract disorder; tumour necrosis factor; TNF; DR3; TR6; TNF-gamma-beta protein; inflammatory bowel disease; Crohn's disease; ulcerative colitis; TRAIL; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tumor necrosis factor gamma-beta antagonists for treating or rating a disease or disorders of the gastrointestinal tract, natory bowel disease, Crohn's disease or ulcerative colitis.
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ABW02276 standard; protein; 281
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9803-0005020
9803-0014047P
9803-00131237
9903-0131963P
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2001US-00899059.
2001US-0314381P.
2001US-0336695P.
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2000US-00559290.
2000US-0216879P.
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N-PSDB; AAD63912.
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08-FEB-1999;
30-APR-1999;
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inflammatory
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                                                                                                                                                      Human TRAIL
                                                                                                   12-FEB-2004
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Length 281; Indels

Score 1478; DB 7; Pred. No. 3.8e-137;

1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE 60

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The invention relates to a composition comprising several CDNAs that are differentially expressed in a liver disorder. The composition is useful for treating liver disorder such as hyperlipidaemia, hypertenaton, type I diabetes, tumours of the liver and disorders of the inflammatory and immune response. The composition is useful for a high-throughput method of screening several molecules or compounds to identify a ligand which specifically binds a cDNA. A protein encoded by the cDNA is useful for a high-throughput method for using a protein to screen several molecules or compounds to identify at least one ligand which specifically binds the protein which involves combining the protein encoded by the cDNA with several of molecules or compounds under conditions to allow specific binding, and detecting specific binding between the protein and a molecule or compound, therefore identifying a ligand which specifically confides the protein. The composition is useful for detecting and quantifying differential gene expression, can be used in gene therapy, to formulate prognosis and to design a treatment regimen and to monitor the
                                                                                                                                 180
                                                                                                                                                                                                       240
                                                                                                                                                                                                                                         240
                                                                                         DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Composition comprising several cDNAs that are differentially expressed in
treated human C3A liver cell cultures, useful for treating liver
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human, liver disorder, hyperlipidaemia, hypertension, type II diabetes, tumour; liver, inflammatory disorder; immune response disorder; high-throughput screening; differential gene expression; gene therapy.
RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
                                                                                                                                                                                                                          DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ
                                                                                                                                                                 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
                                                                                                                                                                                                       FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDFILLMKSARNSCWSKDAEYGLY
                                                                                                                                                                                                                                                                             SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
                                                                                                                                                                                                                                                                                                SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human protein expressed in a liver disorder #32.
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                                                                                                                                                                                                                                                                                                                                                                                                        ADE76953 standard; protein; 281 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-JUL-2000; 2000US-0222113P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-JUL-2001; 2001US-00919039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2004-031227/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (KASE/) KASER M R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; ADE76952.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                          ADE76953;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              substituted by Val or Leu at referred to in claim 17"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "wild-type Asp may be substituted by Asn, Glu or
Gln at this location in the variant referred to in claim
17"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cytostatic, antiarthritic, neuroprotective, gene therapy, Apo-2 ligand, variant, cancer, immune system disease, arthritis, multiple sclerosis;
efficacy of treatment. The present sequence represents the amino acid sequence of a protein encoded by a cDNA differentially expressed in a liver disorder.
                                                                                                                                                                                                                                                   61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ
                                                                                                                                                                                                                                                                                                    121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
                                                                                                                                                                                                                                                                                                                                                                181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLLMKSARNSCWSKDAEYGLY
                                                                                                                                                                                      1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
                                                                                                                                                                                                                     DDSYWDPNDEESMNSPCWQVKWQLRQLVRKM1LRTSEETISTVQEKQQNISPLVRERGPQ
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                                                                                                                                                                                                                                                                                                                                                FYY I YSQTYFRFQEEI KENTKNDKQMVQY I YKYTSYPDPI LLMKSARNSCWSKDAEYGLY
                                                                                                                                                           1 MAMMEVOGGPSLGOTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 substituted by Arg, Asp, location in the variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "wild-type Gln may be substituted by Arg
location in the variant referred to in claim 17"
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                                                                                           Length 281;
                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                            SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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                                                                                           100.0%; Score 1478; DB 8;
100.0%; Pred. No. 3.8e-137;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "wild-type His may be
Asn, Ala, Pro or Thr at this
referred to in claim 17"
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this location in the variant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-MAY-2004 (first entry)
                                                                                                           Sest Local Similarity 100. Atches 281; Conservative
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                                                               Sequence 281 AA;
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31-DEC-2003

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The invention relates to a novel isolated Apo-2 ligand variant polypeptide. Comprising a sequence that differs from the native sequence Apo-2 ligand polypeptide sequence comprising 882 amino acids and having one or more following amino acid substitutions at the residue positions comprising S96C, S101C, S111C, R170C or K179C. Also disclosed is an isolated nucleic acid molecule comprising the Apo-2 ligand variant polypeptide. Further disclosed are a composition comprising the Apo-2 ligand variant polypeptide in mammalian cells. The Apo-2 ligand variant polypeptide is useful for preparing a composition for treating cancer, and method of inducing apoptosis in mammalian cells. The Apo-2 ligand variant polypeptide is useful for preparing a composition for treating cancer or immune-related disease, e.g., arthritis or multiple sclerosis. The current sequence represents the human Apo-2 ligand amino acid sequence. Note: The variant sequence that is referred to in claim 17 may contain one or more of the potential substitutions highlighted in the features
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DDSYMDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
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                                                                                                                                                                                                    New Apo-2 ligand variant polypeptide, useful for preparing a composition for treating cancer or immune-related disease, e.g., arthritis or multiple sclerosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 1478; DB 8; Length 281; 100.0%; Pred. No. 3.8e-137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                   Lindstrom SH
                                                                                                                                                                                                                                                                                            Claim 17; SEQ ID NO 1; 111pp; English
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                                                      24-JUN-2002; 2002US-0391050P.
                  23-JUN-2003; 2003WO-US019750
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 100.
Matches 281, Conservative
                                                                                                                                 Hymowitz S, Kelley RF,
                                                                                           (GETH ) GENENTECH INC
                                                                                                                                                                      WPI; 2004-082490/08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 281 AA;
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The invention relates to a novel isolated Apo-2 ligand variant polypeptide, comprising a sequence that differs from the native sequence Apo-2 ligand polypeptide sequence comprising 282 amino acids and having one or more following amino acid substitutions at the residue positions comprising S96C, S101C, S111C, R170C or K179C. Also disclosed is an isolated nucleic acid molecule comprising DNA encoding the Apo-2 ligand variant polypeptide. Further disclosed are a composition comprising the Apo-2 ligand variant polypeptide, a method of treating cancer, and a method of finducing apoptosis in mammalian cells. The Apo-2 ligand variant polypeptide is useful for preparing a composition for treating cancer or immune-related disease, e.g., arthritis or multiple sclerosis. The current sequence represents the human Apo-2 ligand amino acid sequence. Note: The variant sequence the human Apo-2 ligand amino acid sequence.
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                                                                                Cys at this
                                                                                                                                                                                     at this
                                                                                                                                                                                                                                     /note= "wild-type Arg may be substituted for Cys at this location in the variant referred to in claim 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gand variant polypoptide, useful for preparing a composition cancer or immune-related disease, e.g., arthritis or
                                                                                                                                  at this
                                                                                                                                                                                                                                                                                           at this
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                                                                                                                                  may be substituted for Cys of referred to in claim 1"
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                                                                              /note= "wild-type ser may be substituted for location in the variant referred to in claim
                                                                                                                                                                                                                                                                                       /note= "wild-type Lys may be substituted for location in the variant referred to in claim
                                                                                                                                                                                     /note= "wild-type ser may be substituted for location in the variant referred to in claim
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Pred. No. 3.8e-137;
); Mismatches 0;
                                                                                                                                                    location in the variant referred
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                                                                                                                                  /note= "wild-type ser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 1; 111pp; English.
                                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                               24-JUN-2002; 2002US-0391050P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GETH ) GENENTECH INC
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                                                                                                                                                                    Misc-difference 111
                                                                                                                  Misc-difference 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          multiple sclerosis.
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Best Local Similarity
Marches 281; Conser
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                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hymowitz S,
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The invention relates to a novel isolated Apo-2 ligand variant polypeptide, comprising a sequence that differs from the native sequence Apo-2 ligand polypeptide sequence comprising 282 amino acids and having one or more following amino acid substitutions at the residue positions comprising S96C, S101C, S111C, R170C or K179C. Also disclosed is an isolated nucleic acid molecule comprising DNA encoding the Apo-2 ligand variant polypeptide. Further disclosed are a composition comprising the Apo-2 ligand variant polypeptide, and enchod of treating cancer, and a method of inducing apoptosis in mammalian cells. The Apo-2 ligand variant polypeptide a composition for treating cancer or
                  181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Val
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "wild-type Gln may be substituted by Arg, Ser,
Thr, Val or Lys at this location in the variant referred
to in claim 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gand variant polypeptide, useful for preparing a composition cancer or immune-related disease, e.g., arthritis or
                                                                                                                                                                                                                                                                                                                                                                                                                                                by Ala at this
                                                                                                                                                                                                                                                                                                                Cytostatic; antiarthritic; neuroprotective; gene therapy, Apo-2 ligand; variant; cancer; immune system disease; arthritis; multiple sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "wild-type Asn may be substituted by Gly, Lys, or Arg at this location in the variant referred to in claim 2"
 FYY I YSQTYFRFQEEIKENTKNDKQMVQY I YKYTSYPDPILLMKSARNSCWSKDAEYGLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ala,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "wild-type Lys may be substituted by His, Ala Arg, Gly, Thr or Ser at this location in the variant referred to in claim 2"
                                                                                                                                                                                                                                                                                 Human Apo-2 ligand with potential substitutions highlighted #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                            note= "wild-type Tyr may be substituted by A location in the variant referred to in claim
                                                                                241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
                                                                SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lindstrom SH;
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                                                                                                                                                                                ADK72304 standard; protein; 281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kelley
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multiple sclerosis.
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181
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                                                                                                                                                                                                                                                                                   RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
                                                                                                                                                                                                                                                                                                                        240
                                                                                                                                                                                                                                                                                                                                                 240
immune-related disease, e.g., arthritis or multiple sclerosis. The current sequence represents the human Apo-2 ligand amino acid sequence. Note: The variant sequence that is referred to in claim 2 may contain one or more of the potential substitutions highlighted in the features table
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                                                                                                                                                                          MAMMEVOGGPSLGOTCVLIVIFTVLLOSLCVAVTYVYFTNELKOMODKYSKSGIACFLKE
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                                                                                                      Score 1478; DB 8;
Pred. No. 3.8e-137;
); Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 1; 111pp; English
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                                                                                                    Query Match
Best Local Similarity 100.
Matches 281, Conservative
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for treating cancer or im
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GETH ) GENENTECH INC
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Misc-difference
                                                                               Sequence 281 AA;
                                                    for this record.
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The invention relates to a novel isolated Apo-2 ligand variant polypeptide, comprising a sequence that differs from the native sequence Apo-2 ligand polypeptide sequence comprising 282 amino acids and having one or more following amino acid substitutions at the residue positions comprising S96C, S101C, S111C, R170C or K179C. Also disclosed is an isolated nucleic acid molecule comprising DNA encoding the Apo-2 ligand variant polypeptide. Further disclosed are a composition comprising the Apo-2 ligand variant polypeptide, a method of treating cancer, and a method of inducting apoptosis in mammalian cells. The Apo-2 ligand variant polypeptide is useful for preparing a composition for treating cancer or immune-related disease, e.g., arthritis or multiple sclerosis. The current sequence represents the wild-type human Apo-2 ligand amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSETISTVQEKQQNISPLVRERGPQ 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cytostatic, antiarthritic; neuroprotective; gene therapy, Apo-2 ligand, variant, cancer; immune system disease; arthritis; multiple sclerosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
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Pred. No. 3.8e-137;
Mismatches 0;
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/note= "wild-type His may be substituted by Ala, His, Gly, Gln, Asp, Arg, Pro, Ser, Glu, Asn or Lys at this

Misc-difference

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The invention relates to a novel isolated Apo-2 ligand variant polypeptide, comprising a sequence that differs from the native sequence to Apo-2 ligand bolypeptide sequence comprising 282 amino acids and having one or more following amino acid substitutions at the residue positions comprising S96C, 5101C, 5111C, R170C or K179C. Also disclosed is an isolated nucleic acid molecule comprising DNA encoding the Apo-2 ligand variant polypeptide. Further disclosed are a composition comprising the Apo-2 ligand variant polypeptide, a method of treating cancer, and a method of inducing apoptosis in mammalian cells. The Apo-2 ligand variant polypeptide is useful for preparing a composition for treating cancer or immune-related disease, e.g., arthritis or multiple sclerosis. The current sequence represents the human Apo-2 ligand amino acid sequence. Note: The variant sequence that is referred to in claim 10 may contain and for this record
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                                                                                            /note= "wild-type Asp may be substituted by Ser, Glu,
Gln, Asp or Asn at this location in the variant referred
to in claim 10"
269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gand variant polypeptide, useful for preparing a composition cancer or immune-related disease, e.g., arthritis or
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                                    /note= "wild-type Ile may be substituted by Leu, Met or val at this location in the variant referred to in claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MAMMEVQGGPSLGGTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
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                                                                                                                                                                                   /note= "wild-type Asp may be substituted by Ser, Asn, Asp, Ala, Arg or Glu at this location in the variant referred to in claim 10"
location in the variant referred to in claim 10"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Score 1478; DB 8;
; Pred. No. 3.8e-137;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lindstrom SH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 10; SEQ ID NO 1; 111pp; English.
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Best Local Similarity 100.
Matches 281; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New Apo-2 ligand variant
                                                                                                                                                                                                                                                                                                                                                                                                             (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cable for this record
                                                                                            Misc-difference 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2004-082490/08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                multiple sclerosis.
                     Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 281 AA;
                                                                                                                                                                   Misc-difference
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241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

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The invention relates to apoptosis inducing molecule-I protein (AIM-I)

comprising sequence that is 70 % identical to AD53976 or its mature form
where the polypeptide binds antibody specific to AIM-I, induces apoptosis
of cell line derived from pathological tissue and induces apoptosis of
cells. Also included are a composition comprising AIM-I and a carrier,
AIM-I produced by a process involving expressing in a host cell a nucleic
acid that encodes the protein so as to produce the protein (where the
cucleic acid is chosen from a polynucleotide encoding AIM-I, mature AIM-
cucleic acid is chosen from a polynucleotide encoding AIM-I, mature AIM-
cucleic acid is chosen from a polynucleotide that is complementary to
complete the protein so as to sequence encoded by human cDNA contained in
ATCC Deposit No. 9448, and a polynucleotide that is complementary to
consisting of 0.5 x SSC (Saline-Sodium Citrate) and 0.1 % sodium dodecyl
sulphate (SDS) to a polynucleotide chosen from polynucleotide encoding
mature/AIM I, and a polynucleotide chosen from polynucleotide encoding
contained in ATCC Deposit No. 97448, where the
by human cDNA contained in ATCC Deposit No. 97448, where the
colynucleotide encodes a polypoptide that has the sme biological
cattivity as described above). AIM-I is useful for treating
colynucleotide above). AIM-I is useful for treating
colynucleotide above). AIM-I is useful for treating
colynucleotide chosens, graft versus host disease, for
consisting peripheral tolerance, destroying pathologic transformed cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel apoptosis inducing molecule polypeptide that induces apoptosis of cell line derived from pathological tissue and induces apoptosis of T cells, useful for treating lymphadenopathy, autoimmune diseases and graft
                                                                                                                                                                            Human; apoptosis inducing molecule 1; AIM-1; apoptosis; autoimmune disease; graft versus host disease; lymphadenopathy; immunosuppressive; vasotropic; cytostatic; peripheral tolerance; cell activation; cell proliferation; immune regulation; inflammatory response; systemic lupus erythematosus; inflammatory disease; neoplasm; tumour; restenosis.
                                                                                                                                                                                                                                                                                                                                                                                                                            39. .281
/label= Mature AIM 1
/note= "Claimed in claim 1"
                                                                                                                                       Human apoptosis inducing molecule 1, AIM-1.
                                                                                                                                                                                                                                                                                                                                                                                                         "Signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 2; 36pp; English.
                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                   A
                ADJ63976 standard; protein; 281
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                                                                                                 (first entry)
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'note=
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13-MAR-1997;
                                                                                                 20-MAY-2004
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                                                           ADJ63976;
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                                                                                                                                                                                                                                                                                                                                                                                     Peptide
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ADJ6397
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lines, mediating cell activation and proliferation. AIM-1 proteins are functionally linked as primary mediators of immune regulation and inflammatory response, are useful for diagnosis and treatment of disorders of cells, tissues and organisms. AIM-1 is useful as research tool in elucidating biology of autoimmune disorders including systemic lupus erythematosus, immunoproliferative disease lymphadenopathy and is useful for inhibiting neoplasia such as tumour cell growth. AIM-1 is also useful to treat diseases which required growth promotion activity e.g., restenosis. AIM-1 is useful for assessing AIM-1 binding capacity of its binding molecules such as receptor molecules. The present sequence
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                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Apoptosis inducing molecule-I; AIM-I; cell activation; cell differentiation; apoptosis; autoimmune disease; graft-versus-host disease; lymphadenopathy; gene therapy; human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human apoptosis inducing molecule-I (AIM-I) protein.
                                                                                                                                                                                                                                          100.0%; Score 1478; DB 8;
100.0%; Pred. No. 3.8e-137;
ive 0; Mismatches 0;
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97US-00816981.
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                                                                                                                                                                                                                                                           Best Local Similarity 100.
Matches 281; Conservative
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                                                                                                                                                                          represents AIM-1.
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                                                                                                                                                                                                          Sequence 281 AA;
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ADL71816
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                                                The invention relates to antibodies specific to apoptosis inducing molecule-I (AIM-I) polypeptides. The invention is useful in research, biological, diagnostic, clinical or therapeutic applications. It is also used for modulating activation and differentiation of cells, both normally and in disease states, or for mediating apoptosis and preventing or treating autoimmune diseases, graft-versus-host disease or lymphadenopathy. The invention is also useful in gene therapy. The present sequence is human AIM-I protein.
                                                                                                                                                                                                                                                          DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
                                                                                                                                                                                                                                                                      DDSYMDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
                                                                                                                                                                                                                                                                                                    RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
                                                                                                                                                                                                                                                                                                                 RVAAHITGTRGRSNTLSSPNSKAEALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
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                                                                                                                                                                                                                                                                                                                                                           FYXIXSQTYFRFQEEIKENTKNDKQMVQXIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
                                                                                                                                                                                                                           applications, such as in the treatment of autoimmune diseases or graft-
                                                                                                                                                                                                                 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; TRAIL; TNF related apoptosis inducing ligand; apoptosis;
cytostatic; virucide; tumour necrosis factor; Jurkat cell; cancer;
programmed cell death; leukaemia; colorectal cancer; viral infection;
vaccine.
                                                                                                                                                                                            Gaps
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                                                                                                                                                                      Length 281;
                                                                                                                                                                                          Indels
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                                                                                                                                                                      100.0%; Score 1478; DB 8; 100.0%; Pred. No. 3.8e-137;
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te= "Transmembrane domain"
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/note= "Claimed in claim 7"
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/note= "Cytoplasmic domain"
                                                                                                                                                                                           0; Mismatches
                               Claim 1; SEQ ID NO 2; 36pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 281; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note=
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          versus-host disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human TRAIL protein
                                                                                                                                                  Sequence 281 AA;
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The invention relates to a new purified tumour necrosis factor related apoptosis inducing ligand (TRAIL) polypeptide comprising an amino acid sequence that is at least 9% identical to human TRAIL (ADK15502). The TRAIL polypeptide induces apoptosis of Jurkat cells. Also included are a purified human TRAIL polypeptide encoded by the recombinant vector deposited in strain ATCC 69849 (or a fragment of human TRAIL protein of SEQ ID NO: 2 that induces apoptosis of Jurkat cells), a fusion protein comprising a leucine zipper comprising at least two soluble TRAIL polypeptides (comprising a leucine zipper comprising at least two soluble TRAIL polypeptides (or at least two comprising at least two soluble TRAIL polypeptides (or at least two soluble TRAIL polypeptides (or at least two contacting TRAIL-sensitive cancer cells with a TRAIL polypeptide or with a noligomer defined above). The TRAIL polypeptide is useful in studies of apoptosis, in regulating programmed cell seath, for treating leukaemia, cancer (e.g. colorectal cancer) or viral infections, or in purifying tenkamia cells or adesired cell surface antigen which can be used in evaccine development. The TRAIL polypeptide may also be used in cancer cancer mediated by defective or insufficient amounts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New tumor necrosis factor related apoptosis inducing ligand polypeptides, useful in studies of apoptosis, in regulating programmed cell death, or for treating leukemia, cancer (e.g. colorectal cancer) or viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MAMMEVOGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYPTNELKOMODKYSKSGIACFLKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of TRAIL. The present sequence represents human TRAIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 1478; DB 8;
; Pred. No. 3.8e-137;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 2; SEQ ID NO 2; 42pp; English.
29-JUN-1995; 95US-00496632.
01-NOV-1995; 95US-00548368.
25-JUN-1996; 96US-00670354.
10-NOV-1998; 98US-00190464.
26-MAY-1999; 99US-0019046.
26-MAY-1999; 90US-001320424.
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Best Local Similarity 100.
Matches 281; Conservative
                                                                                                                                                                                                                                                                                                                                           Goodwin RG;
                                                                                                                                                                                                                                                                    (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                              2004-238577/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; ADK15497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   infections
                                                                                                                                                                                                                                                                                                                                           Wiley SR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
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121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to apoptosis inducing molecule I (AIM-I) polypeptide and the encoding polynucleotide useful in biological, diagnostic. Cilifical and therapeutic arts. The invention is useful in treating autoimmune disorders such as systemic lupus erythematosus, immunoproliferative disease lymphadenopathy (IPL), andioimmunoproliferative lymphadenopathy (IPL), rhumatoid arthritis, diabetes and multiple sclerosis, graft versus sost disease, lymphoproliferative disease such as lymphadenopathy, in inhibiting neoplasis such as tumour cell growth, in treating restenosis and regulating haematopoiesis in endothelial cell development. The invention is useful in chromosome identification and as a diagnostic marker for determining expression of AIM-I polypeptide in tumour cell lines including pancreatic tumour, endometrial tumour and T-cell lines invention is also useful in gene therapy. The present sequence is human apptosis inducing molecule I (AIM-I) protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel human apoptosis inducing molecule I useful for treating lymphadenopathy, systemic lupus erythematosus, rheumatoid arthritis and
                                                                                                                                                            Apoptosis inducing molecule I; AIM-I; therapeutic; autoimmune disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                               arthritis
                                                                                                                                                                         systemic lupus erythematosus; immunopoliferative disease lymphadenopathy; IPL; immunopoliferative disease lymphadenopathy; AlL; rheumatoid arthrit: angioimmunoproliferative lymphadenopathy; AlL; rheumatoid arthrit: diabetes; multiple sclerosis; graft versus host disease; lymphacenopathy; neoplasis; lymphacenopathy; neoplasis; tumour cell growth; restenosis; hematopoiesis; chromosome identification; pancreatic tumour; endometrial tumour; T-cell lymphoma; gene therapy; human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 1478; DB 8;
100.0%; Pred. No. 3.8e-137;
ive 0; Mismatches 0;
                                                                                                                      Human apoptosis inducing molecule-1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 2; 35pp; English.
                  ADN07587 standard; protein; 281 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                           16-SEP-2003; 2003US-00662430.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97US-00816981.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96US-0013405P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC.
                                                                                     (first entry)
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281; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         multiple sclerosis.
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                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-MAR-1996;
13-MAR-1997;
                                                                                       17-JUN-2004
                                                                                                                                                                                                                                                                                                                                                                                                          11-MAR-2004
                                                    ADN07587;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ruben SM;
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ADN07587
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Antiarthilic; antitheumatic; agartointestinal-Gen; antiathmatic; antiathmatic; antiathmatic; antiathmatic; antiatheumatic; antiathmatic; antiatheumatic; antiatheumatic; immunosuppressive; vulnerary; gene therapy; immune disorder; witneraps tregulation; cancer; aberrant apoptosic; inflammatory disorder; NP-kappaB regulation; cancer; aberrant apoptosis; wheat: TgM syndrome; hypohidrotic ectodermal dysplasia; whyer-TgM syndrome; hypohidrotic ectodermal dysplasia; wiral infection; HIV-1; HTLV-1; hepatitis B; hepatitis C; EBV; influenza; viral infection; HIV-1; HTLV-1; hepatitis B; hepatitis C; EBV; influenza; where treploated arthritis; inflammatory bowel disease; colitis; asthma; atherosclerosis; cachexia; euthyroid sick syndrome; stroke; EAE; autoimmune disorder; hyper immune activity; where tresponse; hypercongenital condition; birth defect; mercontic lesion; wound; organ transplant rejection; where transduction; proliferating disorder; cancer;
                     RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
                                                                               240
                                                                                                     FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention relates to the novel association of protein sequences (and the genes which encode them) to the NF-kappaB pathway. The invention may be useful for the production of compounds with an antinilammatory, cytostatic, hepatotropic, virucide, antiarthritic, antirheumatic, gastrointestinal-Gen, antiasthmatic, antiarteriosclerotic, immunosubpressive or vulnerary activity or for gene therapy. The proteins and nucleotides are useful for diagnosing, preventing, treating, or ameliorating conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NF-kappaB pathway; antiinflammatory; cytostatic; hepatotropic; virucide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated polynucleotides and polypeptides associated with NF-kappaB pathway, useful for diagnosing, treating, or preventing disorders or diseases associated with NF-kappaB pathway.
RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
                                                                               FYY I Y SQTYFR F QEEIKENTKNDK QMV QY I YKYTS YPDPILLMKSARNSCWSKDAEYGLY
                                                                                                                                                                SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
                                                                                                                                                                                          SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
                                                                                                                                                                                                                                                                                                                                                                                                                                            Human NF-kappaB pathway-associated protein SeqID210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 6; SEQ ID NO 210; 237pp; English.
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                                                                                                                                                                                                                                                                                                               ADR14209 standard; protein; 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BRIM ) BRISTOL-MYERS SQUIBB CO.
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12-MAY-2003; 2003US-0469757P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-JAN-2004; 2004WO-US000798
                                                                                                                                                                                                                                                                                                                                                                                                  21-OCT-2004 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               propagation; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2004-562168/54.
N-PSDB; ADR14208.
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                                                                                                                                                                                                                                                                                                                                                        ADR14209;
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immune disorder, an inflammatory disorder, an inflammatory disorder related to aberrant NP-kappaB regulation, cancer, aberrant apoptosis, related to aberrant NP-kappaB regulation, cancer, aberrant apoptosis, confers, hopeful disorders, Hodgkin's Lymphomas, haematopoietic tumours, hyper-IgM syndromes, hypohidrotic ectodermal dysplasia, x-linked anhidrotic ectodermal dysplasia, immunodeficiency, viral infections, HIV-1, HTLV-1, confermal dysplasia, immunodeficiency, viral infections, HIV-1, HTLV-1, conversival, evasion of immune responses, rheumatoid arthritis, inflammatory bowel disease, colitis, asthma, atherosclerosis, cachexia, euthyroid sick bowel disease, colitis, asthma, atherosclerosis, cachexia, euthyroid sick converse, stroke, BAR, autoimmune disorderse, disorders related to hyper immune activity, disorders related to aberrant acute phase responses, hypercongenital conditions birth defects, necrotic lesions, wounds, cygan transplant rejection, conditions related to organ transplant cristion birth defects, necrotic lesions, wounds, crejection, disorders related to aberrant signal transplant conditions. The present sequence is that of a human protein which is subject to the novel association with the NF-kappaB pathway of the invention. Note: This sequence does not appear in the specification but was obtained by the indexer from Genbank.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FYYIYSQTYPRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLLMKSARNSCWSKDAEYGLY 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antibody; VH domain; VL domain; TR4 binding antibody; TRAIL receptor; haematological cancer; cytostatic; immunotherapy; Non-Hodgkin's lymphoma; chronic myelogenous lymphoma; multiple myeloma; chronic lymphocytic leukaemia; scFv; human; TRAIL; TNP-related apoptosis-inducing ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FYYIYSQTYFRFQEEIKENTKNDKQWVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MAMMEVQEGPSLEGTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE 60
diseases associated with the NF-kappaB pathway. The condition is an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 1478; DB 8; Length 281; 100.0%; Pred. No. 3.8e-137; tive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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Matches 281; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 281 AA;
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15-AUG-2002; 2002US-0403382P. 13-NOV-2002; 2002US-0425730P.

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The present invention describes an antibody or its fragment comprising a VH and VL domain that is at least 80% identical to a VH and a VL domain of any of the 14 sequences given in SEQ ID NO:43 to 56, or a VH and a VL domain of an antibody expressed by any one of the cell lines contained in American Type Culture Collection (ATCC) Deposit numbers PTA-3571, PTA-3570 and PTA-3575, where the antibody specifically binds TR4 (TRAIL receptor). Also described is a pharmaceutical composition for treating or preventing haematological cancer, comprising the antibody or its fragment and member selected from ibritumomab tiuxetern, imatinib mesylate, bortezomid, and a smac peptide or polypeptide. The antibody has cytostatic activity, and can be used in immunotherapy. The antibody or its fragment can be used for the preparation of a pharmaceutical composition for treating or preventing haematological cancer, e.g. Non-Hodgkin's lymphoma, chronic myelogenous lymphoma, multiple myeloma, or chronic myelogenous lymphoma, multiple myeloma, or tumour necrosis factor (TMP) related apoptosis-inducing ligand (TRAIL), which is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
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                                                                                                                                                             Use of an antibody or its fragment the specifically binds to TR4, for t preparation of a pharmaceutical composition for treating or preventing hematological cancer, e.g. Non-Hodgkin's lymphoma, multiple myeloma or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNBLKQMQDKYSKSGIACFLKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tumour inhibition; tumour treatment; metastasis; infectious lesion; antigen presenting cell; immunostimulatory cytokine; cytostatic; vulnerary; immunomodulator; melanoma; hepatoma; adenocarcinoma;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 1478; DB 8; Length 281; 100.0%; Pred. No. 3.8e-137; Live 0; Mismatches 0; Indels 0.
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                                                                                Albert VA;
                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 66; 353pp; English.
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                                                                                Rosen CA,
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06-MAY-2003; 2003US-0468050P.
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                                                                                Ruben SM,
                                         HUMAN GENOME
                                                                                                                        WPI; 2004-203784/19
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Matches 281;
                                                                                Salcedo T,
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Human, cancer-associated protein, cytostatic, cancer, leukaemia, lymphoma; CAP.

Human cancer-associated protein HP7-053.3.

18-NOV-2004 (first entry)

AB084415;

ABO84415 standard; protein; 281 AA.

AB084415

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tumour, metastasis or infectious leaton in a subject which comprises
administering into or near a site of a tumour or infectious lesion in a
subject an antigen presenting cell and an immunostimulatory cytokine or a
nucleic acid encoding the cytokine. The invention may be useful for the
production of compounds with a cytostatic or vulnerary activity acting as
immunomodulators. The method is useful in inhibiting or treating as
tumour, metastasis or infectious lesion in a subject, where the size of
the tumour, metastasis (where number is also decreased) or infectious
ce the tumour, metastasis (where number is also decreased) or infectious
ce is denocarcinoma, colorectal cancer, basal cell cancer, oral cancer,
cancer, renal cancer, laryngeal cancer, bladder cancer, head and neck
cancer, renal call cancer, pancreatic cancer, pulmonary cancer, cervical
cancer, ovarian cancer and breast cancer. The present sequence is that
cell a protein which is related to the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Inhibiting or treating a tumor, metastasis or infectious lesion comprises administering into or near site of a tumor or infectious lesion an antigen presenting cell and an immunostimulatory cytokine or a nucleic
colorectal cancer; basal cell cancer; oral cancer; nasopharyngeal cancer; laryngeal cancer; bladder cancer; head cancer; neck cancer; renal cell cancer; pancratic cancer; pulmonary cancer; cervical cancer; ovarian cancer; oseophageal cancer; pastric cancer; prostrate cancer; testicular cancer; breast cancer; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention relates to a novel method of inhibiting or treating a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 36; 169pp; English
                                                                                                                                                                                                                                                       15-OCT-2003; 2003WO-US032827
                                                                                                                                                                                                                                                                                              15-OCT-2002; 2002US-0418865P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     encoding the cytokine
                                                                                                                                                                                                                                                                                                                                          (UYPI-) UNIV PITTSBURGH
                                                                                                                                                                                                                                                                                                                                                                                 Tahara H;
                                                                                                                                                                                                                                                                                                                                                                                                                             2004-365083/34.
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                                                                                                                                                                    WO2004034995-A2
                                                                                                                              Homo sapiens.
                                                                                                                                                                                                               29-APR-2004
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Best Local 8
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New isolated cancer-associated polynucleotides and polypeptides useful for diagnosing, preventing or treating cancers, especially lymphoma and leukemia, or in screening for agents that modulate cancer.

claim 18; seqid 36; 310pp; English.

Malandro MS;

Morris DW,

Morris DW,

WPI; 2004-652914/63. N-PSDB; ABD32555

; 2003US-00388838. ; 2003US-00417375. ; 2003US-00461862. ; 2003US-00663431.

14-MAR-2003; 2 15-APR-2003; 2 13-JUN-2003; 2 15-SEP-2003; 2

2003US-00737318

(SAGR-) SAGRES DISCOVERY INC

2003US-00367094

14-FEB-2003;

17-FEB-2004; 2004WO-US004730

WO2004074320-A2

02-SEP-2004.

Homo sapiens.

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The invention relates to an isolated nucleic acid comprising at least 10 in the specification, or its complement. The nucleic acids encode cancerassociated proteins. Also included are an expression vector comprising the isolated nucleic acid cited above, a host cell comprising the above cereombinant nucleic acid cited above, a host cell comprising the above cereombinant nucleic acid cited above, a host cell comprising the above cereombinant nucleic acid cited above, a host cell comprising the above central contiguous nucleotides of any of the above comprising at least 10 contiguous nucleotides of any of the above central contiguous nucleotides of a CA sequence sa mentioned in the specification, or its opportunity in isolated antibody, (or its antigen binding fragment) that binds to the above polypeptide, a hybridoma that produces the above monoclonal antibody, a pharmaceutical composition comprising the above monoclonal antibody, a pharmaceutical cancer cells in an individual, a method for inhibiting growth of cancer cells in an individual, a method for inhibiting growth of cancer cells in an individual, a method for inhibiting growth of cancer cells in a ni individual, an electronic library comprising the above polymetride (or their fragments), methods of sereening for anticancer activity or for a bloactive agent capable of modulating the activity of a CA protein (CAP) methods for detecting cancer cells in a method for treating cancers and a method for inhibiting the expression of a polymetric associated with expression of a polymetric and methods are useful for detecting, cancer cells in method for treating cancers and a method for inhibiting cancers, especially lymphoma and lankaemia. These may also be used in screening cancer is
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100.0%; Pred. No. 3.8e-137;
ive 0; Mismatches 0;
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Matches 281; Conservative

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                                                                                                                                                                                                                                                    RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
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                                                                                                                                              1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
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                                                                                             Indels
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                                                            100.0%; Score 1478; DB 8;
100.0%; Pred. No. 3.8e-137;
ive 0; Mismatches 0;
at ftp.wipo.int/pub/published_pct_sequences
                                                    Query Match
Best Local Similarity 100.
Matches 281; Conservative
                                Sequence 281 AA;
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PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive; osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic; antiasthmatic; hepatotropic; respiratory; gene therapy; immune system. Ş standard; protein; 281 polypeptide SEQ ID NO:566. (first entry) 18-NOV-2004 ADP23388; ADP23388 PRO ADP23386 RESULT

30-OCT-2003; 2003WO-US034312. 01-NOV-2002; 2002US-0423394P. 21-MAY-2004.

WO2004041170-A2

Unidentified

(GETH) GENENTECH INC

Clark H, Schoenfeld J, Wu TD;

Wood WI;

Williams PM,

Van Lookeren M,

2004-419628/39. N-PSDB; ADP23387 WPI;

New PRO polypeptides and polynucleotides, useful for treating e.g. erythematosus, rheumatoid arthritis, diabetes mellitus, immune-mediated renal disease, or demyelinating diseases of the central or peripheral nervous system

Claim 7; SEQ ID NO 566; 2940pp; English

polypeptide encoded by it. A protein of the invention has antiliflammatory, antilaribrit, antilhematic, immunosuppressive, osteopathic, antidiabetic, dermatological, antipsoriatic, antiallergic, antidiabetic, and respiratory activity. A polynucleotide antissthmatic, hepatotropic, and respiratory activity. A polynucleotide The invention relates to a novel isolated nucleic acid and the PRO

cut the inventious may nave a use in gene therapy, the kwo polypeptide, the agonist, antagonist, or antibody that specifically binds to the polypeptide is useful for treating an immune related disorder such as systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, osteoarthritis, osteoarthritis, osteoarthritis, osteoarthritis, osteoarthritis, osteoarthritis, osteoarthritis, systemic systemic conversity, autoimmune haemolytic anaemia, autoimmune haemolytic anaemia, autoimmune haemolytic anaemia, autoimmune haemolytic anaemia, autoimmune chromania, thyroiditis, diabetes mellitus, immune-mediated renal disease, a demyelinating disease of the central or peripheral nervous system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome, contention inflammatory demyelinating polyneuropathy, a hepatobilary disease, infectious or autoimmune chronic active hepatitis, primary cirlosis, granulomatous hepatitis, sclerosing cholangitis, inflammatory bowel disease, granulomatous hepatitis, sclerosing cholangitis, disease, an autoimmune or immune-mediated skin disease, a bullous skin disease, asthma, allergic rhinitis, atopic dermatitis, food disease, asthma, allergic rhinitis, atopic dermatitis, food disease, asthma, allergic rhinitis, atopic dermatitis, food chaemistivity uricaria, an immunologic disease of the lung, costinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity preminents a transplantation associated disease, graff rejection or of the invention polypeptide, its The PRO invention may have a use in gene therapy. of the invention

Sequence 281 AA;

240 120 DDSYMDPNDEESKMSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120 180 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180 9 9 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDFILLMKSARNSCWSKDAEYGLY Gaps .. 0 Length 281; Indels SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281 ; Score 1478; DB 8; ; Pred. No. 3.8e-137; 0; Mismatches 0; 100.08; 100.08; Conservative Query Match Best Local Similarity Matches 281; Conserv 61 61 121 181 241 8 ò 셤 ò g 용 ð 셤 ð ઠ

SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

completed: June 3, 2005, 12:09:44 Job time : 166 secs Search

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June 3, 2005, 11:53:43; Search time 54 Seconds (without alignments) 1798.816 Million cell updates/sec
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(cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB. PEP: *

(cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB. PEP: *

(cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB. PEP: *

(cgn2_6/ptodata/1/pubpaa/PCTUG_PUBCOMB. PEP: *

(cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB. PEP: *

(cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB. PEP: *

(cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB. PEP: *

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(cgn2_6/ptodata
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1465611 segs, 345679903 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Published_Applications_AA:*
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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1478
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                                                                                                                                                                                                                                                                                                                     Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		,			COLUMNICO		
Result		Query					
No.	Score	Match	Match Length DB	DB	ID	Description	
1	1478	100.0	281	80	US-08-916-625B-6	Sequence 6, Appli	
~	1478	100.0		ω	US-08-971-317A-8	Sequence 8, Appli	
m	1478	100.0		σ	US-09-813-329-17	Sequence 17, Appl	
4	1478	100.0		σ	US-09-193-663-8	Sequence 8, Appli	
S	1478	100.0		σ	US-09-934-465-1	Sequence 1, Appli	
v	1478	100.0		10	US-09-919-039-118	Sequence 118, App	
7	1478	100.0		13	US-10-011-125-4	Sequence 4, Appli	
60	1478	100.0		13	US-10-001-054-54	Sequence 54, Appl	
σ	1478	100.0		14	US-10-093-766-54	Sequence 54, Appl	
10	1478	100.0		14	US-10-174-654-11	11,	
11	1478	100.0	281	14	US-10-151-882-41	Sequence 41, Appl	
12	1478	100.0		14	US-10-218-547-20	Sequence 20, Appl	
13	1478	100.0		14	US-10-322-673-72	Sequence 72, Appl	

equence 66 equence 26 equence 8,	9,4,9,4	Sequence 2, Appli Sequence 2, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli	4,4,0,0	3, 23, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,	9179	Sequence 4, Appl. Sequence 5, Appl. Sequence 14, Appl. Sequence 6, Appl. Sequence 6, Appl.
US-10-139-785- US-10-310-793- US-10-279-687-	US-10-293 US-10-333 US-10-662	15 US-10-662-431-2 15 US-10-662-430-2 15 US-10-652-244-2 16 US-10-381-160-5 16 US-10-755-889-210	US-10-491-326-1 US-10-771-254-1 US-10-855-559-2 US-10-451-200-5	US-10-495-353- US-10-652-979- US-10-066-209- US-10-367-094- US-10-978-203-	2 - 5 4 4 A B B B B B B B B B B B B B B B B B	15 US-10-389-223A-4 18 US-10-389-223A-2 14 US-10-185-425-5 9 US-09-855-544A-14 10 US-09-873-829-6 11 US-10-017-910-6
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777	44444	1478 1478 1478 1478	1471	11 1 1 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	1269.1 101. 988 988.1	982 978 978 937.5 930 930
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ALIGNMENTS

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Sequence 6, Application US/08916625B

Publication No. US20010010924A1

GENERAL INFORMATION:
APPLICANT: DEEN, KEITH C.
APPLICANT: YOUNG, PETER R.
TITLE OF INVENTION: TUMOR NECROSIS PACTOR RELATED
TITLE OF INVENTION: RECEPTOR, TR6
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: RAINER & PRESTIA
STREET: P.O. BOX 980
CITY: VALLEY FORGE
STATE: PA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                           ZUDIATE BADABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: DISKETE
COPTWARE: FastSEQ for Windows Version 2.0
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/916,625B
FILING DATE: 22-Aug-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/853,684
FILING DATE: 09-MAY-1997
FILING DATE: 14-MARCH-1997
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
REGISTRATION NUMBER: 23,031
REGISTRATION NUMBER: GH-50008-1
TELECOMMUNICATION INFORMATION:
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USA
US-08-916-625B-6
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TOPOLOGY:
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US-08-971-317A-8
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                                                                                                                                                                                                     100.0%; Score 1478; DB 8;
100.0%; Pred. No. 1.3e-128;
tive 0; Mismatches 0;
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Publication No. US20010010925A1

GENERAL INFORMATION:

APPLICANT: Wiley, Steven R.

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

TUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSE: Abbott Laboratories

STREET: 100 Abbott Park Road

CITY: Abbott Park

STATE: IL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDLUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: Fast-SEQ for Windows Version 2.0b
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/971,317A
FILING DATE: 17-NOV-1997
FILING DATE: APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6255.US.01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INPORMATION:
NAME: GOller, Mimi C
REGISTRATION NUMBER: 39,046
REFERENCE/DOCKET NUMBER: 6255
TELECOMMUNICATION INFORMATION:
TELEPAK: (847) 938-7550
TELEFAK: (847) 938-2623
TELEX:
TELEPAONE: 610-407-0700
TELEFAX: 610-407-0701
TELERS: 846169
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS: LENGTH: 281 amino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear NOLECULE TYPE: protein
                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 281; Conservative
                                                                                                                                                                      US-08-916-625B-6
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APPLICANT: Bristol-Myers Suibb Company
TITLE OF INVENTION: No. US20020012968Alel Drosophila Tumor Necrosis Factor Class Mole
TITLE OF INVENTION: Variants Thereof
FILE REFERENCE: D0016.mp
CURRENT APPLICATION NUMBER: US/09/813,329
CURRENT APPLICATION NUMBER: US/09/813,329
PRIOR FILING DATE: 2001-03-20
PRIOR PILING DATE: 2000-03-21
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PatentIn version 3.0
SEQ ID NO 17
LENGTH: 281
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0
                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 1478; DB 8; Length 281; Best Local Similarity 100.0%; Pred. No. 1.3e-128; Matches 281; Conservative 0; Mismatches 0; Indels 0;
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100.0%; Score 1478; DB 9;
Best Local Similarity 100.0%; Pred. No. 1.3e-128;
Matches 281; Conservative 0; Mismatches 0;
                                                                                                                                                                                    MOLECULE TYPE: No. US20010010925Ale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 17, Application US/09813329; Patent No. US20020012968A1; GENERAL INFORMATION:
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US-09-813-329-17
                         SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: amino acid
STRANDEDNESS: single
INFORMATION FOR SEQ ID NO:
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Best Local Similarity
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181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
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                                                                                                                                       Sequence 8, Application US/09193663

Patent No. US20020055624A1

GENERAL INFORMATION:

TITLE OF INVENTION: TNP-DELTA LIGAND AND USES THEREOF

FILE REFERENCE: 6255.US.02

CURRENT APPLICATION NUMBER: US/09/193,663

CURRENT APPLICATION NUMBER: 60/065,916

EARLIER PILLING DATE: 1998-11-17

EARLIER FILLING DATE: 1997-11-17

NUMBER OF SEQ ID NOS: 10

SOFTWARE: FASTSEQ for Windows Version 3.0
                              SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
                                               241 SIYOGGIFELKENDRIFVSVTNBHLIDMDHEASFFGAFLVG 281
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Patent No. US20020102233A1
GENERAL INPORMATION:
JAPLICANT: ABANEMBATION:
JATTLE OF INVENTION: APO-2 LICAND
FILE REFERENCE: 11669.22US03
CURRENT APPLICATION NUMBER: US/09/934,465
CURRENT FILING DATE: 2001-08-21
PRIOR FILING DATE: 1996-01-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 281
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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US-09-934-465-1
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APPLICANT: Kaser, Matthew R.

TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES FILE REFERENCE: PA-0035 US CURRENT APPLICATION NUMBER: US/09/919,039
CURRENT PILING DATE: 2002-09-09
PRIOR PPLING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 401
SOFTWARE: PERL Program
SEQ ID NO 118
LENGTH: 281
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Best Local Similarity 100.0%; Pred. No. 1.3e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030108871A1 059509CD1
US-09-919-039-118
                           Indels
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100.0%; Pred. No. 1.3e-128; ative 0; Mismatches 0;
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                         Matches 281; Conservative
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ORGANISM: Homo sapiens
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RESULT

100.0%; Score 1478; DB 9; Length 281;

Query Match

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PRIOR PILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/08149
PRIOR APPLICATION NUMBER: 60/08659
PRIOR PILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: 60/09689
PRIOR PILING DATE: 1998-06-11
PRIOR PILING DATE: 1998-06-25
PRIOR PILING DATE: 1998-06-17
PRIOR PILING DATE: 1998-06-17
PRIOR PILING DATE: 1998-06-17
PRIOR PILING DATE: 1998-06-17
PRIOR PILING DATE: 1998-09-10
PRIOR PILING DATE: 1998-09-10
PRIOR PILING DATE: 1998-09-10
PRIOR PILING DATE: 1998-09-15
PRIOR PILING DATE: 1999-01-12
PRIOR PILING DATE: 1999-01-13
PRIOR PILING DATE: 19
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APPLICANT: Genentech, inc.

APPLICANT: Goddard, Audrey

APPLICANT: Goddard, Audrey

APPLICANT: Goddard, Audrey

APPLICANT: Goddard, Audrey

APPLICANT: Henzel, William

APPLICANT: Henzel, William

APPLICANT: Smith, Victoria

APPLICANT: Watenabe, Colin

APPLICANT: Watenabe, Watenabe,
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100.0%; Score 1478; DB 13;
Best Local Similarity 100.0%; Pred. No. 1.3e-128;
Matches 281; Conservative 0; Mismatches 0;
US-10-011-125-4

Sequence 4, Application US/10011125

Publication No. US20020142388A1

GENERAL INFORMATION:

APPLICANT: Chen, Christina Yu-Ching

TITLE OF INVENTION: BACTERIAL HOST STRAINS

FILE REFERENCE: P1804R1

CURRENT APPLICATION NUMBER: US/10/011,125

CURRENT PILING DATE: 2001-12-07

PRIOR RILING DATE: 2000-12-14

NUMBER OF SEQ ID NOS: 10

SEQ ID NO 4
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Publication No. US20020192209A1
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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Best Local Similarity
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240 180 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120 181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPIILLMKSARNSCWSKDAEYGLY 240 Sequence 54, Application US/10093766

Publication No. US20030013099A1

GENERAL INFORMATION:

APPLICANT: Lasek, Amy W.

APPLICANT: Jones, David A.

APPLICANT: WITH JONES, David A.

TITLE OF INVENTION: GENES REGULATED BY DNA METHYLATION IN COLON TUMORS

FILE REFERENCE: PA-047 US

CURRENT APPLICATION NUMBER: US/10/093,766

CURRENT PILING DATE: 2002-03-07

NUMBER OF SEQ ID NOS: 61

SOFTWARE: PERL PROGRAM

SEQ ID NO 54

LENGTH: 281 9 DDSYMDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE Gaps ö ; Score 1478; DB 13; Length 281; ; Pred. No. 1.3e-128; 0; Mismatches 0; Indels 0; ; NAME/KEY: misc_feature ; OTHER INFORMATION: Incyce ID No. US20030013099A1 059509CD1 US-10-093-766-54 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281 PRIOR APPLICATION NUMBER: PCT/USO1/06520
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: PCT/USO1/06666
PRIOR APPLICATION NUMBER: PCT/USO1/17092
PRIOR FILING DATE: 2001-03-01
PRIOR FILING DATE: 2001-06-25
PRIOR FILING DATE: 2001-06-01
PRIOR PLILNG DATE: 2001-06-01
PRIOR PLILNG DATE: 2001-06-01
PRIOR PLILNG DATE: 2001-06-20
PRIOR PLILNG DATE: 2001-06-20
PRIOR PLILNG DATE: 2001-06-29
PRIOR PLILNG DATE: 2001-07-09
PRIOR PLILNG DATE: 2001-07-09
PRIOR PLILNG DATE: 2001-07-09
PRIOR APPLICATION NUMBER: PCT/USO1/27099
PRIOR PLILNG DATE: 2001-07-09
PRIOR PLILNG DATE: 2001-07-09 100.0%; 100.0%; Matches 281; Conservative TYPE: PRT ORGANISM: Homo sapiens FEATURE: ; TYPE: PRT ; ORGANISM: Homo Sapien US-10-001-054-54 Query Match Best Local Similarity ð 유 ò 용 8 용

DB 14; Length 281;

100.0%; Score 1478;

Query Match

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RESULT 12
US-10-218-547-20
US-00-218-547-20
| Publication No. US20030100074A1
| GENERAL INFORMATION:
| APPLICANT: Human Genome Sciences, Inc.
| TITLE OF INVENTION: Methods And Compositions For Treating Metabolic Bone Diseases Rel
                                                                                                                                                                                           120
                                                                                    DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
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US-10-151-882-41
US-10-151-882-41
Sequence 41, Application US/10151882
Publication No. US20030058862A1
GENERAL INFORMATION:
TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
FILE REFERENCE: PF554
CURRENT APPLICATION NUMBER: US/10/151,882
CURRENT FILING DATE: 2002-05-22
PRIOR APPLICATION NUMBER: 60/293,100
PRIOR FILING DATE: 2010-05-24
PRIOR FILING DATE: 2010-05-24
NUMBER OF SEQ ID NOS: 48
SOCTIVARE: Patentin version 3.0
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Best Local Similarity 100.0
Matches 281; Conservative
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CORGANISM: Homo sapiens
US-10-151-882-41
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LENGTH: 281
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Legal Services
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COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 Diskette

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/174,654

FILING DATE: 19-JUM-2002

CLASSIFICATION: «Unknown»

ATTORNEY/AGENT INFORMATION:
                     Indels
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100.0%; Score 1478; DB 14;
Best Local Similarity 100.0%; Pred. No. 1.3e-128;
Matches 281; Conservative 0; Mismatches 0;
100.0%; Pred. No. 1.3e-128; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 11, Application US/10174654
Publication No. US20030044937A1
GENERAL INFORMATION:
APPLICANT: Bienkowski, Michael J
Mills, Cynthia J
JONES, David A
TITLE OF INVENTION: TNF-Related Death Ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Kerber, Lori L.
REGISTRATION NUMBER: 41,113
REFERENCE/DOCKET NUMBER: 6111.N CN1
TELECOMMUNICATION INFORMATION:
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SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-174-654-11
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TYPE: amino acid
STRANDEDNESS: single
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TELEFAX: 616/833-8897
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Best Local Similarity 100.
Matches 281; Conservative
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STATE: MI
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US-10-174-654-11
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HITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL

TITLE OF INVENTION: Receptors

FILE NUMBERISHER RECEPTORS

CURRENT FILING DATE: 2002-05-07

FRICH PAPLICATION NUMBER: 60/369,860

FRICH APPLICATION NUMBER: 60/340,860

FRICH RILING DATE: 2001-04-05

FRICH FILING DATE: 2001-11-2

FRICH FILING DATE: 2001-11-3

FRICH FILING DATE: 2001-11-14

FRICH FILING DATE: 2001-11-07

FRICH FILING DATE: 2001-11-07

FRICH FILING DATE: 2001-11-07

FRICH FILING DATE: 2001-11-07

FRICH APPLICATION NUMBER: 60/331,044

FRICH FILING DATE: 2001-10-07

FRICH FILING DATE: 2001-10-07

FRICH FILING DATE: 2001-09-21

FRICH FILING DATE: 2001-09-21

FRICH FILING DATE: 2001-09-21

FRICH FILING DATE: 2001-06-04

FRICH FILING DATE: 2001-06-05

FRICH FILING DATE: 201-06-05

FRICH FILING DATE: 2001-06-05

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                0; Indels
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                Mismatches
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Publication No. US20030190685A1
GENERAL INFORMATION:
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CORGANISM: Homo sapiens
US-10-139-785-66
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APPLICANT: Salcede et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL

TITLE OF INVENTION: Receptors

FILE REFERENCE: PFS85

CURRENT APPLICATION NUMBER: US/10/322,673

CURRENT PILING DATE: 2002-12-19

PRIOR PLICATION NUMBER: 60/341,237

PRIOR FILING DATE: 2001-12-20

PRIOR FILING DATE: 2001-12-20

PRIOR FILING DATE: 2002-04-05

PRIOR PRIOR DATE: 2002-04-05

PRIOR PLING DATE: 2002-04-05

PRIOR PLING DATE: 2002-04-05

PRIOR PLING DATE: 2002-06-04

PRIOR PLING DATE: 2002-06-04

PRIOR PLING DATE: 2002-06-05

PRIOR PLING DATE: 2002-06-15

PRIOR PLING DATE: 2002-11-13

NUMBER OF SEQ ID NOS: 72

LENGTH: 281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 281;
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100.0%; Pred. No. 1.3e-128;
tive 0; Mismatches 0;
TITLE OF INVENTION: Human Endokine Alpha FILE REFERENCE: PF561
CURRENT APPLICATION NUMBER: US/10/218,547
CURRENT FILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: 60/312,542
PRIOR PILING DATE: 2001-08-16
PRIOR PILING DATE: 2001-08-16
PRIOR FILING DATE: 2001-08-16
NUMBER: OF SEQ ID NOS: 57
SEQ ID NO 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 72, Application US/10322673; Publication No. US20030180296A1; GENERAL INFORMATION:
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Matches 281; Conservative
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US-10-322-673-72
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                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: human
US-10-218-547-20
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PAPELICANT: Salcedo et al.

TITLE OF INVENTION: Antibodies That Immunospecifically Bind To TRAIL Receptors
TITLE OF INVENTION: Antibodies That Immunospecifically Bind To TRAIL Receptors
TITLE OF INVENTION: WHOBER: US/10/292,486
CURRENT APPLICATION NUMBER: US/10/392,486
CURRENT PILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: 60/403,376
PRIOR PLIING DATE: 2002-08-15
PRIOR FILING DATE: 2002-08-07
PRIOR FILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: 60/331,309
  61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
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APPLICANT: Wiley, Steven R.
TITLE OF INVENTION: TNF-DELTA LIGAND AND USES THEREOF
FILE REPERENCE: 6255.US.C2
CURRENT APPLICATION NUMBER: US/10/279,687
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: US 10/105,738
PRIOR FILING DATE: 2002-03-25
PRIOR FILING DATE: 1998-11-17
PRIOR PILING DATE: 1998-11-17
PRIOR FILING DATE: 1998-11-17
PRIOR FILING DATE: 1998-11-17
PRIOR PILING DATE: 1998-11-17
NUMBER: OF SEQ ID NOS: 10
SOFTWARE: FASTEEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                       ; Sequence 8, Application US/10279687; Publication No. US20030211509A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/10292486; Publication No. US20030228309A1; GENERAL INFORMATION:
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                                                                                                                                                                                                                                  RESULT 16
US-10-279-687-8
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Publication wo. US20030198640A1
Sequence 26, Application US/10310793
Publication wo. US20030198640A1
Sequence 26, Application wo. US20030198640A1
Sequence 26, Application wo. US20030198640A1
Sequence 27, Turus OP INVENTION: Methods And Compositions For Treating Inflammatory Bowel Diseases
TITLE OF INVENTION: Methods And Compositions For Treating Inflammatory Bowel Diseases
TITLE OF INVENTION: Methods And Compositions For Treating Inflammatory Bowel Diseases
TITLE OF INVENTION: Methods And Compositions For Treating Inflammatory Bowel Diseases
TITLE OF INVENTION: Methods And Compositions For Treating Inflammatory Bowel Diseases
TITLE OF INVENTION WHERE: US/10/316, 595
PRIOR FILING DATE: 2001-12-06
PRIOR FILING DATE: 2001-08-32
PRIOR FILING DATE: 2001-03-66
PRIOR PLILNG DATE: 2000-04-06
PRIOR PLILNG DATE: 2000-04-06
PRIOR PLILNG DATE: 2000-04-06
PRIOR APPLICATION WHERE: 60/124,067
PRIOR APPLICATION WHERE: 60/124,067
PRIOR APPLICATION WHERE: 60/122,27
PRIOR PLILNG DATE: 2000-04-03
PRIOR PLILNG DATE: 2000-04-04
PRIOR PLILNG DATE: 2000-04-04
PRIOR PLILNG DATE: 2000-04-04
PRIOR PLILNG DATE: 2000-04-04
PRIOR PLILNG DATE: 1999-06-03
PRIOR PLILNG DATE: 1999-06-03
PRIOR PLILNG DATE: 1999-06-03
PRIOR PLILNG DATE: 1999-06-03
PRIOR PLILNG DATE: 2000-04-04
PRIOR PLILNG DATE: 2000-04-
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61 DDSYWDPNDEESWNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
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Best Local Similarity 100.
Matches 281; Conservative
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ORGANISM: human
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181 FYYIYSQTYFRPQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
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                                                                                                                           61 DDSYMDPNDEESMNSPCWQVKWQLRQLVRKKMILRTSEETISTVQEKQQNISPLVRERGPQ
                                                                                                                                                                                                                    1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
                                                                                                    61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ
                                                                                                                                                                                        121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
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           1 MAMMEVOGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/10662429;
Publication No. US20040038347A1
GENERAL INFORMATION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS: 1
STREET: 9410 Key West Avenue
CITY: Rockville
STRATE: MAD
                                                                                                                                                                                                                                                                                                                                                                    241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
                                                                                                                                                                                                                                                                                                                                                                                                241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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PLING DATE: 13-WAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Kimball, Paul, C.
REGISTRATION NUMBER: 34,610
REFERENCE/DOCKET NUMBER: PF261
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/662,429
FILING DATE: 16-Sep-2003
CLASSIPICATION: 530
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 2:
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Publication No. US20040005314A1

GENERAL INFORMATION:

APPLICANT: Escandon, Enrique

APPLICANT: Fox, Judith A.

APPLICANT: Kelley, Sean K.

APPLICANT: Xiang, Hong

TILE REPERENCE: P1838R1

CURRENT APPLICATION NUMBER: US/10/333,712

CURRENT APPLICATION NUMBER: US/10/333,712

CURRENT PILING DATE: 2001-07-27

PRIOR FILING DATE: 2001-07-27

PRIOR FILING DATE: 2000-07-27

NUMBER OF SEQ ID NOS: 4

SEQ ID NO 1

SEQ ID NO 1
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; Pred. No. 1.3e-128;
0; Mismatches 0;
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PRIOR FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 09/986,149
PRIOR FILING DATE: 2001-110-07
PRIOR APPLICATION NUMBER: 60/327,359
PRIOR FILING DATE: 2001-10-09
PRIOR PELING DATE: 2001-06-04
PRIOR PILING DATE: 2001-06-04
PRIOR PILING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-16
PRIOR PLING DATE: 2000-11-08
NUMBER OF SEQ ID NOS: 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 281; Conservative
                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-486-5
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ORGANISM: Homo Sapien
US-10-333-712-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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61 DDSYMDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
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                                                                                 COMPUTER LEADING GISK
COMPUTER: FLORDY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/662,431
FILING DATE: 16-Sep-2003
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/816,981
ATTORNEY/AGENT INFORMATION:
NAME: Kimball, Paul, C.
REGISTRATION NUMBER: 34,610
REFERENCE/DOCKET NUMBER: PF261
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 1478; DB 15;
100.0%; Pred. No. 1.3e-128;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:

LENGTH: 281 amino acids
TYPE: amino acid
TYPE: Jinear

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
US-10-662-431-2
                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 2:
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                           COUNTRY: US
ZIP: 20850
COMPUTER READABLE FORM:
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COMPUTER READABLE FORM:
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Best Local Similarity 100.
Matches 281; Conservative
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US-10-662-430-2
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DSYMDPNDEESMASPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGFQ 120
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                                                                                                                                                                                                                                                                                                                                                                             Sequence 200, Application US/1020262

| Sequence 200, Application US/1020262
| Publication No. US20040038349A1
| GENERAL INFORMATION:
| APPLICANT: Human Genome Sciences, Inc.,
| TITLE OF INVENTION: Heteromultimeric TNF Ligand Family members
| FILE REPERENCE: PFS59
| CURRENT APPLICATION NUMBER: US/10/202,062
| CURRENT APPLICATION NUMBER: 60/307,838
| PRIOR APPLICATION NUMBER: 60/307,838
| PRIOR FILING DATE: 2001-07-27
| NUMBER OF SEQ ID NOS: 42
| SOFTWARE: PatentIn version 3.0
| SEQ ID NO 20
| LENGTH: 281
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US-10-662-431-2
; Sequence 2, Application US/10662431
; Publication No. USZO040047864A1
; GENERAL INFORMATION:
APPLICANT: Ruben, Steven M
TITLE OF INVENTION: Apoptosis Inducing Molecule I
NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                          US-10-202-062-20
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Sequence 5, Application US/10381160
Publication No. US20040131587A1
APLICANT: INFORMATION:
TITLE OF INVENTION: METHOD FOR TREATMENT OF TUMORS USING COMBINATION THERAPY
TITLE OF INVENTION: METHOD FOR TREATMENT OF TUMORS USING COMBINATION THERAPY
TITLE OF INVENTION: METHOD FOR TREATMENT OF TUMORS USING COMBINATION THERAPY
CURRENT PREDICATION NUMBER: US/10/381,160
CURRENT PELING DATE: 2003-03-17
PRIOR APPLICATION NUMBER: US 60/242,868
PRIOR APPLICATION NUMBER: US 60/242,868
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 FYYIYSQTYFRFQEEIKENTKNDKQWVQXIXKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
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100.0%; Score 1478; DB 16; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.3e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                   Length 281;
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100.0%; Pred. No. 1.3e-128;
tive 0; Mismatches 0;
                                  496,632
PRIOR FILING DATE: 1995-11-01
PRIOR APPLICATION NUMBER: 08/499;
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 2;
LENGTH: 281
TYPE: PRT
                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0
Matches 281; Conservative
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ORGANISM: Homo sapiens
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US-10-652-244-2
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LENGTH: 281
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; Sequence 2. Application US/1065244
; Publication No: US20040052788A1
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REPRENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/10/652,244
; CURRENT APPLICATION NUMBER: US/09/796,581
; PRIOR APPLICATION NUMBER: 09/320,424
; PRIOR FILING DATE: 1999-05-26
; PRIOR FILING DATE: 1999-05-26
; PRIOR FILING DATE: 1999-05-36
; PRIOR APPLICATION NUMBER: 09/190,046
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 09/048,641
; PRIOR FILING DATE: 1998-03-26
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 08/670,354
; PRIOR FILING DATE: 1996-06-25
; PRIOR APPLICATION NUMBER: 09/048,641
  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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100.0%; Pred. No. 1.3e-128;
Live 0; Mismatches 0;
                                                                           CURRENT APPLICATION DATA:
RAPLICATION NUMBER: US/10/662,430
FILING DATE: 16-5ep-2003
CLASSIPICATION: 530
                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/816,981
FILING DATE: 13-MAR-1997
                                                                                                                                                                                                                                                ATTORNEY/AGBNT INFORMATION:
NAME: Kimball, Paul, C.
REGISTRATION NUMBER: 34,610
REGISTRATION NUMBER: PF261
TELEPONMUNICATION INFORMATION:
TELEPON: (301) 309-8504
TELEPAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: amino acids
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; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-662-430-2
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Best Local Similarity 100.
Matches 201; Conservative
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APPLICANT: Flores, Heather
APPLICANT: Flores, Heather
APPLICANT: Dai, Tanya P.
APPLICANT: Pai, Tanya P.
APPLICANT: Shahrokh, Zahra
APPLICANT: Matchews, Timochy C.
TILE OF INVENTION: App.2 LIGAND/TRAIL FORMULATIONS
FILE REPERSONCE: P1857R1P1
CURRENT APPLICATION NUMBER: US/10/771,254
CURRENT PILING DATE: 2004-02-03
PRIOR APPLICATION NUMBER: US 60/338,249
PRIOR APPLICATION NUMBER: PCT/US02/36251
PRIOR PILING DATE: 2001-11-13
PRIOR FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 2
SEQ ID NO 1
                                                              100.0%; Score 1478; DB 16;
100.0%; Pred. No. 1.3e-128;
ive 0; Mismatches 0;
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Pred. No. 1.3e-128;
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100.0%; Pred. No. 1...
0; Mismatches
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US-10-771-254-1
i. Sequence 1, Application US/10771254
i. Publication No. US20050020498A1
i. GENERAL INFORMATION:
                                                                                                          Matches 281; Conservative
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Matches 281; Conservative
    ; ORGANISM: Homo Sapiens
US-10-491-326-1
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US-10-771-254-1
                                                                                    Best Local Similarity
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                                                                                                                                                                                                 Sequence 210, Application US/10755889
Publication No. US20040171823A1
GENERAL INFORMATION:
J GENERAL INFORMATION:
J GENERAL INFORMATION:
J TITLE OF INVENTION: PATTWAY
TITLE OF INVENTION: PATTWAY
TITLE OF INVENTION: PATTWAY
CURRENT APPLICATION NUMBER: US/10/755,889
CURRENT PELING DATE: 2004-01-13
FRIOR PELICATION NUMBER: U.S. 60/440,068
PRIOR PELING DATE: 2003-01-14
PRIOR FILING DATE: 2003-05-12
NUMBER OF SEQ ID NOS: 823
SOFTWARE: PATCH PERIOR OF SEQ ID NOS: 823
SEQ ID NO 210
SEQ ID NO 210
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; Sequence 1, Application US/10491326
; Publication No. US20040186051A1
; GENERAL INFORMATION:
    Patin Docket Freview
    APLICANT: Robert F. Kelley, Stephanie H. Lindstrom
    TITLE OF INVENTION: APO-2 Ligand Variants and Uses Thereof
    FILE REFERENCE: P1858R1
; CURRENT APPLICATION NUMBER: US/10/491,326
; CURRENT FILING DATE: 2004-04-01
; PRIOR APPLICATION NUMBER: US 60/326,622
; NUMBER OF SEQ ID NOS: 6
; SEQ ID NO 1
; LENGTH: 281
; TYPE: PRT
                                                            241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
                                                                                    241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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Matches 281; Conservative
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ORGANISM: Homo sapiens
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US-10-755-889-210
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APPLICANT: BAI, ROGET
APPLICANT: SHAHROKH, Zahra
APPLICANT: SHAHROKH, Zahra
APPLICANT: SHAHROKH, Zahra
APPLICANT: MATTHEWS, Timochy
ITILE OF INVENTION: Apo-2 LIGAND/TRAIL FORMULATIONS
FILE REFERENCE: P1857R1
CURRENT APPLICATION NUMBER: US/10/495,353
CURRENT FILING DATE: 2004-05-12
PRIOR APPLICATION NUMBER: PCT/US02/36251
PRIOR APPLICATION NUMBER: US 60/338,249
                                                                  DB 17;
                                                             ; Score 1478; DB 17;
; Pred. No. 1.3e-128;
O; Mismatches O;
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                                                             100.0%;
                                                             Query Match
Best Local Similarity 100.
Matches 281; Conservative
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; ORGANISM: Homo sapiens
US-10-451-200-5
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US-10-495-353-1
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Best Local Similarity
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Publication No. US2050048645A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: METHOD OF TREATING OR PREVENTING DISEASE CHARACTERIZED BY CRYPTOC TITLE OF INVENTION: NEOPERAD SINFECTION
TITLE OF INVENTION: NEOPERAD SINFECTION
TITLE OF INVENTION: NUMBER: US/10/451,200
CURRENT FILING DATE: 2003-06-21
PRIOR APPLICATION NUMBER: US 60/259,653
PRIOR FILING DATE: 2001-01-04
NUMBER: OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.1
SEQ ID NO 5
LENGTH: 281
                                                                                                                                                                                                                           APPLICANT: Harding, Thomas
APPLICANT: Harding, Thomas
APPLICANT: Jooss, Karin
APPLICANT: Jacoss, Karin
APPLICANT: Jacoss, Karin
APPLICANT: Jacoss, Maind
APPLICANT: Donahue, Brian
TITLE OF INVENTION: Method for Treating Cancer By Vector-Mediated Delivery of
TITLE OF INVENTION: One or More Anti-Angiogenic or Proapoptotic Genes
FILE REFERENCE: 3802-094-27
CURRENT APPLICATION NUMBER: US/10/855,559
CURRENT PILING DATE: 2004-05-28
PRIOR FILING DATE: 2003-06-03
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PERESEQ for Windows Version 4.0
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                                                                                                                                                                  ; Sequence 2, Application US/1085559; Publication No. US20050031593A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapien
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LENGTH: 281
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Pred. No. 1.4e-126;
0; Mismatches 0; Indels 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 22, Application US/10367094; Publication No. US20040170982Al; Publication No. US20040170982Al; Publication No. US20040170982Al; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Therapeutic Targets in Cancer; FILE REFRENCE: 529452001500
; CURRENT APPLICATION UNMBER: US/10/367,094
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 203
; SEQ ID NO 22
; SEQ ID NO 22
; LENGTH: 279
; TYPE: PRT
                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99.4%; Score 1469; DB 13;
100.0%; Pred. No. 8.5e-128;
tive 0; Mismatches 0;
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/057,550
PRIOR FILING DATE: 1997-08-29
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 99.3%;
Matches 279; Conservative (
                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 279; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo sapiens
US-10-367-094-22
                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-10-066-209-3
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                                                                                                                                                  LENGTH: 279
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Publication No. US20020115110A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Brigham-Burke, Michael R.
APPLICANT: Young, Peter R.
TITLE OF INVENTION: A METHOD OF IDENTIFYING AGONIST AND
TITLE OF INVENTION: A METHOD OF IDENTIFYING RECEPTORS TRI AND TR2
FILE REFERENCE: GH-50030-D1
CURRENT FILING DATE: 2001-10-25
PRIOR APPLICATION NUMBER: 09/072,993
PRIOR FILING DATE: 1998-05-06
PRIOR FILING DATE: 1998-05-06
PRIOR FILING DATE: 1998-05-06
PRIOR FILING DATE: 1998-05-06
PRIOR PLING DATE: 1998-05-06
PRIOR PLING DATE: 1908-05-06
PRIOR PLING DATE: 100/056,980
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                              241 SIYOGGIFELKENDRIFVSVINEHLIDMDHEASFFGAFLVG 281
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                                                                                                                                                               Sequence 1, Application US/10652979
Publication No. US20050089958A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Schwall, Ralph H.
TITLE REFERENCE: P0978P3C1
CURRENT APPLICATION NUMBER: US/10/652,979
CURRENT FILING DATE: 2003-08-29
PRIOR FILING DATE: 1998-04-15
PRIOR FILING DATE: 1998-04-15
PRIOR FILING DATE: 1998-01-15
PRIOR FILING DATE: 1998-01-16
PRIOR FILING DATE: 1997-01-08
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US-10-652-979-1
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     241
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181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYG-- 238
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                                                                                                                                            RESULT 34
US-10-978-203-23
Sequence 23, Application US/10978203
Sequence 23, Application US/10978203
Shubilcation No. US20050112666A1
GENERAL INFORMATION:
APPLICANT: Chicheportiche, Yves
APPLICANT: Chicheportiche, Yves
FILE REFERENCE: A003
FILE REFERENCE: A003
CURRENT APPLICATION NUMBER: US/10/978,203
CURRENT FILING DATE: 2004-10-29
PRIOR FILING DATE: 1996-00-07
PRIOR PLICATION NUMBER: 60/023,541
PRIOR FILING DATE: 1996-01-18
PRIOR FILING DATE: 1996-10-18
PRIOR FILING DATE: 1996-10-18
PRIOR FILING DATE: 1996-10-18
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 23
LENGTH: 283
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                                       ; TYPE: PRT
; ORGANISM: homo sapien
US-10-978-203-23
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Search completed: June 3, 2005, 12:06:54 Job time : 56 secs

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RESULT 2
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QéjsG canis famil
QéjsG canis famil
QéjsG homo sapien
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Qégyh mus musculu
Q712q3 cyprinus ca
Q60313 mesocricetu
Geber prachydanio
P04924 orycrolagus
Q91214 sigmodon hi
Q91215 cavia porce
Q71114 pagrus majo
P2645 sus scrofa
P2645 us scrofa
P26437 ictalurus p
Q61373 cavia porce
Q71114 pagrus majo
R21363 sus scrofa
P2660 bos taurus
Q91363 occusalichty
P29553 equus caball
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1 TNELKOMODKYSKSGIACFL.....NEHLIDMDHEASFFGAFLVG 243
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09bec4
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Q6JSD9
Q9WV90
Q6J3Q6
TN15_HUMAN
TN14_HUMAN
Q9MJT9
Q1T104_MOUSE
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0080817
088402
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069XA7
0792C7
TNPA RABIT
091ZL4
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091ZL8
1NPA CAVPO
071TUPA PIG
17NPA PIG
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Match Length DB
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Maximum DB seq length: 243
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P01375 homo sapien 66x658 marmota mon P51743 cervus elap P01374 homo sapien P61125 pan troglod 08hzd9 pan troglod 08h2d9 paralichthy P06804 mus musculu P16599 rattus norv 09jm09 marmota mon P33620 papio sp. (08awc9 cyprinus ca 080wc7 peromyscus 09beal tursiops tr	PRELIMINARY; PRT; 214 AA. 10. (TERBELFE] 16, Lested) 10. (TERBELFE] 16, Lest sequence update) 10. (TERBELFE] 17, Lesterian (TERBELFE] 17, Lesterian (TERBELFE] 18, Lesterian (TERBELFE] 18, Lesterian (TERBELFE] 19, Lesterian (TE
TNFA_HUMAN OGK658 TNFA_CEREL TNFB_HUMAN TNFB_HUMAN TNFA_PANTR Q91841 TNFA_MOUSE TNFA_RAT TNFB_MARMO TNFB_MARMO TNFB_MARMO TNFB_MARMO TNFB_MARMO TNFA_TAT	PRELIMINARY; PRT; 214 AA. 10. (TrEMBLrel. 16, Last sequence update) 10. (TrEMBLrel. 16, Last sequence update) 10. (TrEMBLrel. 25, Last annotation update protein. 10. cerio (Zebrafish) (Danio rerio). 10. rerio (Zebrafish) (Danio rerio). 11. Metazoa; Chordata; Craniata; Vertebrat ryqii; Neopteryqii; Teleostei; Ostarioph e; Danio. 12. Danio. 12. Danio. 13. Prysiol. B. Comp. Biochem. 129:475 (Danio rerio). 14. Danio. 15. Danio. 16. Danio. 17. Danio. 18. Danio. 18. Danio. 19. Danio.
	### 16, C. el. 16, C. el. 15, Li el. 25, Li el. 25, Li el. 26, Li chordata; chordata; covary."; ol. B, Cor 7640.1; covary."; land express covary."; land express land expr
32 7 3 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	PRELIMINARY; 01 (TrEMBLrel. 16, D. 03 (TREMBLrel. 16, L. 03 (TREMBLrel. 25, L. et ol.; et ol.
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169 AA; 19274 MW; FDE395B014717B6B CRC64;
                                Query Match
Best Local Similarity
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TISSUE-Liver;
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     SEQUENCE
                                                                                                                                                                                                                                                                                                                                               905190
                                                           Matches
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R GO; GO: 000556; C: emembrane; IEA.

R GO; GO: 0005164; F: tumor necrosis factor receptor binding; IEA.

R GO; GO: 0005164; F: tumor necrosis factor receptor binding; IEA.

R GO; GO: 0000165; P: immune response; IEA.

R GO; GO: 0007165; P: immune response; IEA.

R InterPro; IPR008064; Fras ligand.

R InterPro; IPR008064; Fras ligand.

R InterPro; IPR008064; Fras ligand.

R InterPro; IPR008064; TNF_IME.

R PRIMTY; RR00299; TNF_IME.

R PRIMTY; RR00212; TNF_SULGAND.

R PRIMTY; RR00212; TNF = ubf; 1.

R PROSITE; PS00251; TNF_1: 1.

R PROSITE; PS00251; TNF_1: 1.

R PROSITE; PS0049; TNF_2: 1.

T NON TER 169 169
                                                                                              Name-TNFSF10;
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                            TISSUE-Lung carcinoma;
Polvi A., Ruosaari S., Vendelin J., West A., Saarikko I.,
Reinikainen A., Hollmen J., Laitinen T., Mannila H., Lahesmaa R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fas ligand (Fragment).
Marmota monax (Woodchuck).
Bukarnota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
                                                                                                                                                                                                                                                                                                                                                                                         1 THELKOMODKYSKSGIACFLKEDDSYMDPNDEESMNSPCWQVKWQLRQLVRK 52
                                                                                                                                                                                                                                                                                                                                                                         1 TNELKOMODKYSKSGIACFLKEDDSYWDPNDEESMNSPCWQVKWQLRQLVRK 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Healthy liver;

MEDLINE-20010026; PubMed=10540161;

MEDLINE-20010026; PubMed=10540161;

Hodgson P.D., Grant M.D., Michalak T.I.;

"Perforin and Ras/Ras ligand-mediated cytotoxicity in acute and chronic woodchuck viral hepatitis.";

chronic woodchuck viral hepatitis.";

clin. Exp. Immunol. 118:63-70(1999).

EMBL, AF152368; AAD38387.1; -...

HSSP; P50591; 1DG6.
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06JSD9 PRELIMINARY; PRT; 63 AA.
06JSD9;
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
C6-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Chemokine tumor necrosis factor ligand superfamily member 10
                                                                                                                                                                                                                                                                                                                      Length 63;
                                                                                                                                                                                                                                                                                                                     22.6%; Score 291; DB 2; Length 63 100.0%; Pred. No. 1.4e-16; rative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                           63 AA; 7638 MW; 8F0C7936DA5AA6E6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         169 AA
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01-NOV-1999 (TrEMBLrel. 12, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                EMBL; AY312579; AAR16184.1; -.
                                                                                                                                                                                                                                                                                                                                               52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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Best Local Similarity
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                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                         NCBI_TaxID=9606;
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                                                                                      (Fragment)
                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                           105 NEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKN 164
                                                                                                                                                                                                                                                                                                                            165 DKQMVQYIY-KYTSYPDPILLMK-SARNSC----WSKDAEYGLYSIYQGGIFELKENDR 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          101 NQPLSHKVYVKNSKYPQDLVLMEGKMMYCTTGQMWAR-----SSYLGAVFNFTSNDH 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93 GRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYF 152
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                                                                          Gaps
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Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
R Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
R RBSP, P01375; JA8M.
GO; GO:0005576; C:extracellular; IEA.
GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
GO; GO:0005165; F:tumor necrosis; IEA.
GO; GO:0007165; P:sigmal transduction; IEA.
R GO; GO:0007165; P:sigmal transduction; IEA.
R InterPro; IPR008064; Fas_ligand.
R InterPro; IPR008064; Fas_ligand.
R InterPro; IPR00531; TNF_c
InterPro; IPR006052; TNF_f
InterPro; IPR008083; TNF_f
InterPro; IPR008083; TNF_f
InterPro; IPR008083; TNF_f
InterPro; IPR008083; TNF_f
InterPro; IPR008081; TNF_f
INF SRMART; SM00207; TNF; I.
R PROSITE; PS00201; TNF_1: I.
R PROSITE; PS00201; TNF_1: I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Fas ligand (Fragment).
Canis familiaris (Dog).
Bukaryota, Metazca; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Carnivora; Fissipedia; Canis.
                                                                      43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33;
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ch 13.6%; Score 175.5; DB 2; Length 169; 1 Similarity 27.8%; Pred. No. 1.5e-06; 54; Conservative 39; Mismatches 58; Indels 43.
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05-JUL-2004 (TrEMBLrel. 27, Created)
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CARBOHYD
CARBOHYD
                                                  SEQUENCE
                                                                                              Query Match
Best Local
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                                                                                                                                         Matches
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153 RFQEEIKENTKNDKQMVQYIY-KYTSYPDPILLAMK-SARNSC----WSKDAEYGLYSIY 205
                          48 RGQ-----SCNNKPLNHKVYMRNSKYPQDLMLMEGKIMNYCTTGQMMAR-----SSY 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
TISSUB-Umbilical vein;
MEDLINE-99091541; PubMed-9872942;
Zhai Y., Ni J., Jiang G.-W., Lu J., Xing L., Lincoln C., Carter K.C., Janat Y., Ni J., Yiang G.-W., Lu J., Aggarwal B.B., Ruben S., Li L.-Y., Gentz R., Yu G.-L.;
"VEGI, a novel cytokine of the tumor necrosis factor family, is an angliogenesis inhibitor that suppresses the growth of colon carcinomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBUNIT: Homotrimer (Potential).
-!- SUBCELLULAR LOCATION: Type II membrane protein (Probable).
-!- TISSUE SPECIPICITY: Specifically expressed in endothelial cells.
Detected in placenta, lung, kidney, skeletal muscle, pancreas, spleen, prostate, small intestine and colon.
-!- SIMILARITY: Belongs to the tumor necrosis factor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- FUNCTION: Inhibits vascular endothelial growth and angiogenesis
                                                                                                                                                                                                                                                                                                28-FEE-2003 (Rel. 41, Created)
28-FEE-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Tumor necrosis factor ligand superfamily member 15 (Vascular endothelial cell growth inhibitor) (TNF ligand-related molecule 1).
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70207; 1NE, ...
PS50049; TNE_2; 1.
Glycoprotein, Signal-anchor; Transmembrane.
Glycoprotein, Signal-anchor for type II membrane
13 25 Signal-anchor for type II membrane
protein (Potential).
26 174 Extracellular (Potential).
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                                                                                         206 OGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
                                                                                                                      174 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF039390; AAD08783.1; -.
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PRINTS; PR01234; TNBCROSISECT.
ProDom, PD002012; TNF subf; 1.
SMART; SMO207; TNF; 1.
PROSITE; PS50049; TNF 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P50591; 1D2Q.
Genew; HGNC:11931; TNFSP15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FASEB J. 13:181-189(1999)
                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (in vitro).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MIM; 604052;
                                                                                                                                                                                                                                                         TN15 HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cytokine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
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                                                                                                                                                                                                                                                                                                                   116 WESSRSGHSFLSN-LHLRNGELVIHEKGFYYIYSQTYFRFQ----EEIKENTKNDK--QM 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=98122340; PubMed=9462508; DOI=10.1016/S1074-7613(00)80455-0; Mauri D.N., Ebner R., Montgomery R.I., Kochel K.D., Cheung T.C., Yu G.-L., Ruben S., Murphy M., Eisenberg R.J., Cohen G.H., Spear P.G., Ware C.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "LIGHT, a new member of the TNF superfamily, and lymphotoxin alpha are
ligands for herpesvirus entry mediator.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      169 VQYIYKYT-SYPDPILLMKSARNSCWSKDAEYG---LYSIYQGGIFELKENDRIFVSVTN
                                                                                                                                                                                                                                                                                                                                                                                      42 WE-HELGLAFTKNRMNYTNKFLLIPESGDÝFIYSQVTFRGMTSECSEIRQAGRPNKPDSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TN14_HUMAN STANDARD; PRT; 240 AA.
043557; 075476; 0804789; 0905LD2;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Tumor necrosis factor ligand superfamily member 14 (Herpesvirus entry mediator-ligand) (HVEM-L) (UNQ391/PR0726).
                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21528948; PubMed=11673523;
Granger S.W., Butrovich K.D., Houshmand P., Edwards W.R., Ware C.F.;
"Genomic characterization of LiGHT reveals linkage to an immune
response locus on chromosome 19p13.3 and distinct isoforms generated
by alternate splicing or proteelysis.";
J. Immunol. 167:5122-5128(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Harrop J.A., McDonnell P.C., Brigham-Burke M., Lyn S.D., Minton J., Tan K.B., Dede K., Spampanato J., Silverman C., Hensley P., DiPrinzio R., Emery J.G., Deen K., Eichman C., Chabot-Fletcher M., Truneh A., Young P.R.; "Herpesvirus entry mediator ligand (HVEM-L), a novel ligand for HVEM/TRZ, stimulates proliferation of T cells and inhibits HT29 cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003; Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J., Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P. Eaton D., Foster J., Grimaldi C., Gu Q., Hase P.E., Heldens S., Lewas L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J., Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
                                                                                                                                                                                                                                       18;
N-linked (GlcNAc. . .) (Potential)
N-linked (GlcNAc. . .) (Potential)
CCB83BA7EE673B98 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=98438532; PubMed=9765287; DOI=10.1074/jbc.273.42.27548;
                                                                                                                                                               DB 1; Length 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Butele
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                       48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM 1), AND CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM 2), AND PROCESSING.
                                                                                                                                                       ch 12.4%; Score 160; DB 1; Similarity 35.3%; Pred. No. 3e-05; 49; Conservative 24; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biol. Chem. 273:27548-27556(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=TNFSF14; Synonyms=HVEML, LIGHT;
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      225 EHLIDMDHE-ASFFGAFLV 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |:| | :|||||:
156 ISLVDYTKEDKTFFGAFLL 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM 1).
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                                                                                       20131 MW;
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   56
152 1
174 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
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H-InvDB; HIX0019691; -.

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**X TESUSEPERIALI, **X NEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Chuler G.D., Atausner R.D., Collins F.S., Wagner L., Sheamen C.M., Schuler G.D., A Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaddo M.F., Carahnoi P.J., Prange C., Brownstein M.J., Usdin T.B., Tochiyuki S., Carahnoi P.J., Mullahy S.J., Brownstein M.J., Usdin T.B., Tochiyuki S., Carahnoi P.J., Mullahy S.J., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., AR Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Vilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Helton B., Ketreman M., Madan A., Rodrigues S., Sanchez A., Miting M., Madan A., Young A.C., Shewchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Rodrigues A.C., Grimwood J., Schmutz J., Myers R.M., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., Touchman J.B., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., Touchman J.B., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., Touchman J.B., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., Febersaling to the decoy receptor TNRRSF68 modulates its effects. Activates NFKB, Stimulates the proliferation of T cells, and inhibits growth of the democarcinoma HT-29. Acts as a receptor for Herpes simplex intermed and supplementarial stress of the second of the democarcinoma HT-29. Acts as a receptor for Herpes simplex interminants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a alicense agreement (See http://www.isb-sib.ch/announce/or send an email to license@ibb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=2; Synonyms-LiGHT delta-TM; 1soid=043557-2; Sequence=vSp 06452; TiSoid=043557-2; Sequence=vSp 06452; TiSoid=043557-2; Sequence=vSp 06452; TiSoid=043557-2; Sequence=vSp 06452; TiSoid=043557-2; Sequence=vSp 06452; TiSoid=0451-2; Sequence=vSp 06452; TiSoid=0451-2; Sequence=vSp 06452; TiSoid=0451-2; Sequence=vSp 06452; TiSoid=0451-2; Sequence=vSp 06452; TiSoid=04525; TiSoid=04
Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.-H., Yansura D., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I., Godowski P., Gray A.; "Ithe secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -i- PTM: N-glycosylated.
-i- PTM: The soluble form of isoform 1 derives from the membrane form by proteolytic processing.
-i- SIMILARITY: Belongs to the tumor necrosis factor family.
-i- CAUTION: Ref.5 sequence differs from that shown due to a frameshift in position 178.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Type II membrane protein and secreted (isoform 1); Cytoplasmic (isoform 2).
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INDUCTION: Up-regulated after T-cell activation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=043557-1; Sequence=Displayed;
                                                                                                                                                                                             Dioinformatics assessment.";
Genome Res. 13:2265-2270(2003).
                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: Homotrimer.
                                                                                                                                                                                                                                                                                                                                                       TISSUE=Brain;
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BC018058; AAH18058.1; ALT_FRAME.

HSSP; PO1375; 415... Genew; HGNC:11930; TNFSF14.

EMBL; AF036581; AAC39563.1; -. EMBL; AF064090; AAC25169.1; -. EMBL; AY358812; AAK26160.1; EMBL; AY358812; AAQ89171.1;

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110 GP------LLWE-TQLGLAFLRGLSYHDGALVVTKAGYYYIYSK------ 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     160 ENTKNDKOMVQY------IYKYT-SYPDPILLMKSARNSCWSKDAEYGLY 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 QLHWRLGEMYTRLPDGPAGSWEQLIQERRSHEVNP-----AAHLTGANSSLTGSG 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100 SPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIK 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   147 -----VQLGGVGCPLGLASTITHGLYKRTPRYPEELELLVSQQSPCGRATSSSRVW 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41 QVKWQLRQLVRKMILRTSEETISTVQEKQQN-ISPLVRERGPQRVAAHITGTRGRSNTLS
                                                                                                                                                                                                                                                                                                                                            member 14, membrane form.
Tumor necrosis factor ligand superfamily
                                                                                                                                                                                                                                                                                                                              Tumor necrosis factor ligand superfamily
                     GO, GO:0043027; F:caspase inhibitor activity, IDA.
GO; GO:005102; F:receptor binding; IPI.
GO; GO:0005102; F:receptor binding; IPI.
GO; GO:0005102; F:receptor binding; IPI.
GO; GO:0006917; P:inhibition of appaces activation; IDA.
GO; GO:0001719; P:inhibition of caspase activation; IDA.
GO; GO:00017165; P:signal transduction; NAS.
GO; GO:0043029; P:T-cell proliferation; NAS.
InterPro; IPR006053; TNF amily.
InterPro; IPR006052; TNF family.
InterPro; IPR008083; TNF family.
InterPro; IPR008083; TNF family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fas ligand CD178 (Frament).
Macaca mulatta (Rhesus macaque).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
NCBI_TaxID=9544;
                                                                                                                                                                                                                                                                                                                                                                                      Cytoplasmic (Potential).
Signal-anchor for type II membrane
protein (Potential).
Extracellular (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12.4%; Score 159.5; DB 1; Length 240;
                                                                                                                                                                                                                                                                PROSITE; PS00251; TNF 1; FALSE NEG.
PROSITE; PS50049; TNF 2; 1.
Alternative splicing; Cytokine; Glycoprotein; Signal-anchor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Pred. No. 5e-05;
41; Mismatches 66; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                203 --SIYQGGIFELKENDRIFVSVTNEHLIDM-DHEASFFGAFLV 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49D0BF67E1390B39 CRC64;
                                                                                                                                                                                                                                                                                                                                                                           member 14, soluble form.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Potential.

N-linked (GlcNAc. .).
Missing (in isoform 2).

FrId=VSP_006452.

L -> V (in Ref. 2).

E -> K (in Ref. 2).
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01-077-2002 (TrEMBLrel. 22, Last sequence update)
01-077-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cleavage (Potential).
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                                                                                                                                                                                                       pfam, pF00229, TNF; 1.
PRINTS, PROLIZ24, TNECROSISFCT.
PRODOM; PD002012, TNF subf; 1.
SMART; SM00207; TNF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26351 MW;
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187
102
73
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58
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82
154
102
38
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85 AAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFY 144
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81 152 1
100 1
191 1
239 AA;
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                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 782
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CARBOHYD
SEQUENCE
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       117 ESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIY-KY 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 TSOKHTASSLEKQIGHPSPPPEKKEORKVAHLTG------KPNSRSMPL-----EW 52
                       MEDLINE=22937400; PubMed=14576776;
Arnoult D., Perit F., Lellevie J.D., Lecossier D., Hance A.,
Monceaux V., Ho Tsong Fang R., Huntrel B., Amelsen J.C., Estaquier J.;
"Caspase-dependent and -independent T-cell death pathways in
pathogenic simian immunodeficiency virus infection: relationship to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20165223; PubMed=10700230; DOI=10.1038/73136; Tamada K., Shimozaki K., Chapoval A.I., Zhu G., Sica G., Flies D., Boone T., Hsu H., Fu Y.-X., Nagata S., Ni J., Chen L.; "Modulation of T-cell-mediated immunity in tumor and graft-versus-host disease models through the LIGHT co-stimulatory pathway."; Nat. Med. 6:283-289(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                          GO: GO:0005576; C:extracellular; IEA.
GO: GO:000526; C:membrane; IEA.
GO: GO:0005164; F:tumor necrosis factor receptor binding; IEA.
GO: GO:000515; P:apoptosis; IEA.
GO: GO:0007155; P:immune response; IEA.
GO: GO:0007165; P:immune response; IEA.
InterPro; IPRO80664; Pas ligand.
InterPro; IPRO80664; Pas ligand.
InterPro; IPRO80698; TNF family.
InterPro; IPRO80898; TNF like.
InterPro; IPRO80898; TNF like.
InterPro; IPRO80898; TNF like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           176 TSYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVT 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12.2%; Score 157; DB 2; Length 154; 27.4%; Pred. No. 4.5e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65; Indels
                                                                                                                                        Hance A.J., Lecossier D., Estaquier J.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF530076; AAM95636.1; -.
HSSP; P50591; 1D2Q.
                                                                                                                                                                                                                                                                                                                                                                                                                         154 154
154 AA; 17410 MW; 971A43779E029449 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Tumor necrosis factor ligand superfamily member 14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33; Mismatches
                                                                                         disease progression.";
Cell Death Differ. 10:1240-1252(2003)
                                                                                                                                                                                                                                                                                                                                           PRINTS; PRO1681; FASLIGAND.
ProDom; PD002012; TNF subf; 1.
SMART; SM00207; TNF, 1.
PROSITE; PS500251; TNF 1; 1.
PROSITE; PS50049; TNF 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=Tnfsf14; Synonyms=LIGHT;
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
            SEQUENCE FROM N.A.
                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46;
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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Best Local (
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TO 4 MOUSE
TO 29 PTH9
DT 28 - FEB
DT 05 - JUL
DE TUNNE=T
GN Mume=T
OC Mume=T
OC Mume=T
OC NO I I I
RN REDLIN
RA TAMAGUIR
RA MOGUIR
RA MAGUIR
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Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Tumor necrosis factor ligand superfamily member 14, soluble form.
Cytoplasmic (Potential).
Signal-anchor for type II membrane protein (Potential).
Extracellular (Potential).
Cleavage (Potential).
Cleavage (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MUCD; MCI:135317; Thefil4.

GO: GO: 0043027; F: Caspase inhibitor activity; ISS.
GO: GO: 0043027; F: Caspase inhibitor activity; ISS.
GO: GO: 0005102; F: receptor binding; ISS.
GO: GO: 000119; P: inhibition of caspase activation; ISS.
GO: GO: 0001165; P: signal transduction; ISS.
GO: GO: 0007165; P: Signal transduction; ISS.
GO: GO: 0043098; P: T-cell proliferation; ISS.
INTERPROSONORS: TNP abc.
InterPro; IPR00693; TNP family.
InterPro; IPR00893; TNP like.
InterPro; IPR08693; TNP subf.
SEQUENCE FROM N.A.

TISSUE-Fetal liver;

MEDLINE-20354998; PubMed=10894944;

Misawa K., Nosaka T., Kojima T., Hirai M., Kitamura T.;

Misawa K., Nosaka T., Kojima T., Hirai M., Kitamura T.;

Misawa K., Dosaka T., Kojima T., Hirai M., Kitamura T.;

Misawa K., Nosaka T., Kojima T., Hirai M., Kitamura T.;

Misawa K., Nosaka T., Kojima T., Hirai M., Kitamura T.;

Misawa K., Nosaka T., Kojima T., Hirai M., Kitamura T.;

Misawa K., Nosaka T., Kojima T., Hirai M., Kitamura T.;

Misawa K., Nosaka T., Kojima T., Hirai M., Kitamura T.;

Misawa K., Nosaka T., Kojima T., Hirai M., Kitamura T.;

Misawa K., Nosaka T., Kojima T., Hirai M., Kitamura T.;

Misawa K., Nosaka T., Kojima T., Hirai M., Kitamura T.;

Misawa K., Nosaka T., Kojima T., Hirai M., Kitamura T.;

Misawa K., Nosaka T., Kojima T., Hirai M., Kitamura T.;

Misawa K., Nosaka T., Kojima T., Hirai M., Kitamura T.;

Misawa K., Nosaka T., Kojima T., Hirai M., Kitamura T.;

Misawa K., Nosaka T., Kojima T., Hirai M., Kitamura T.;

Misawa K., Nosaka T., Kojima T., Hirai M., Kitamura T.;

Misawa K., Nosaka T., Kojima T., Hirai M., Kitamura T.;

Misawa K., Nosaka T., Kojima T., Hirai M., Kitamura T.;

Misawa K., Nosaka T., Kojima T., Hirai M., Kitamura T.;

Misawa K., Nosaka T., Kojima T., Hirai M., Kitamura T.;

Misawa K., Nosaka T., Kojima T., Hirai M., Kitamura T.;

Misawa K., Nosaka T., Kojima T., Hirai M., Kitamura T.;

Misawa K., Nosaka T., Kojima T., Hirai M., Kitamura T.;

Misawa K., Nosaka T., Misawa 
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N-linked (GlcNAc. . .) (Potential)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     proteolytic processing.
--- SIMILARITY: Belongs to the tumor necrosis factor family.

    -!- PTM: The soluble form derives from the membrane form by

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PROSITE; PS00231; TNF_1; FALSE_NEG.
PROSITE; PS50049; TNF 2; Signal-anchor; Transmembrane;
Cytokine; Glycoprotein; Signal-anchor; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, AF123385, AAF76453.1; -. EMBL, AB028155; BAA88559.1; -. EMBL, AF227533; AAF36722.1; -. HSSP, PO1375; 4TSV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS, PR01234; TNECROSISFCT.
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Gaps

25; Mismatches 72; Indels 17;

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Mammalia, Eutheria,
    Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                         NCBI_TaxID=10036;
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NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q6U817;
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Q6U817
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93 AAHLTGANASLIGIGGP-----LLWE-TRLGLAFLRGLTYHDGALVTWEPGYY 139
                                                                 140 YVYSKVOLS-GVGCPQGLANGLPITHGLYKRTSRYPKELELLVSRKSPCGRANSSRVWWD 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75 LVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNG 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                135 ELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPD-----PILLMKSA 188
                                         YIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTS-YPDPILLMKSARNSCWSKDAEYGLY- 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67 LSKENVTSKVAIHLSGA-----YEPDVSKNNIDWKQNQDGAFVSGGLKLVDR 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        114 EIIIPNDGIYFIYSQVSFHI--SCKNDMTEDQEVMHVSHAVFHYSDFFGIYKP--LIRAA 169
                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Head kidney;

TISSUE=Head kidney;

X PubMed=15145420; DOI=10.1016/j.fsi.2003.11.001;

X Savan N.;

X Savan N.;

X Savan N.;

Y Expence of multiple isoforms of TNF alpha in carp (Cyprinus carpio IT.): genomic and expression analysis.";

I Fish Shellifish Immunol. 17.87-94(2004).

R GO; GO:0005164; Extumor necrosis factor receptor binding; IEA.

R GO; GO:0005164; F: ttumor necrosis factor receptor binding; IEA.

R GO; GO:0005164; F: ttumor necrosis factor receptor binding; IEA.

R GO; GO:0006555; P: immune response; IEA.

R InterPro; IPR006952; TNF family.

R InterPro; IPR008983; TNF family.

R InterPro; IPR008983; TNF family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RNSCW----SKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHL--IDMDHEASFFGAF 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31; Gaps
                                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Cyprinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68; Indels
                                                                                             203 SIYQGGIFELKENDRIFVSVTNEHLI-DMDHEASFFGAFLV 242
                                                                                                            | : ||: |: : : | | SSFLGGVVHLEAGEEVVVRVPGNRLVRPRDGTRSYFGAFMV 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NF 2; 1.
25226 MW; 010BC2B1E8D7265E CRC64;
                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
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Last annotation update)
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Best Local Similarity 25.3%; Pred. No. 0.00021;
Matches 45; Conservative 34; Mismatches 68
                                                                                                                                                                                         227 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              216 AA.
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01-AUG-1998 (TrEMBLrel. 07, Last sequency of 1-OCT-2003 (TrEMBLrel. 25, Last annotate)
Tumor necrosis factor-alpha (Fragment).
Mesocricetus auratus (Golden hamster).
                                                                                                                                                                                                                01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last seq
01-MAR-2004 (TrEMBLrel. 26, Last ann
                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                      Name=TNF-3alpha;
Cyprinus carpio (Common carp).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00229; TNF; 1. —
ProDom; PD002012; TNF subf; 1. SMART; SM00207; TNF; 1. SMOSTE; PS50049; TNF 2; 1. SEQUENCE 227 AA; 25226 MW;
                                                                                                                                                                                                                                                         Tumor necrosis factor-3 alpha.
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                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                     NCBI TaxID=7962;
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49 GPOREEKFPNPIIGSMGOTLTLRSSSONSNDKPVGHVVANHQVEEQLEWLSHRANALLAN 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        109 GMSLKDNQLVIPADGLYLVYSQVLFRGQ------GCPSYVLLTHTVSRIAVSYED 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80 GPQRVAAH---ITGTRGRSNTL-SSPNSKNEKALGRKINS-----WESSRSGHSFLS
                                                                                                                                                                                                                                  Melby P.C., Tryon V.V., Chandrasekar B., Freeman G.L.;
"Cloning of Syrian hamster (Mesocricetus auratus) cytokine cDNAs and
analysis of cytokine mRNA expression in experimental visceral
leishmaniasis.";
Infect. Immun. 66:2135-2142(1998).
EMBL; AF046215; AAC40100.1; -.
HSSP; P06804; ZTNF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 PILLMKSARNSCWSKDAEYG----LYSIYQGGIFELKENDRIFVSVTNEHLID 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R GO; GO: 0016020; C: membrane; IEA.
R GO; GO: 0016050; F: tumor necrosis factor receptor binding; IEA.
GO; GO: 0006955; P: tumor necrosis factor receptor binding; IEA.
GO; GO: 0006955; P: tumor necrosis factor receptor binding; IEA.
R InterPro; IPR006053; TNF abc.
R InterPro; IPR006029; TNF anily.
R InterPro; IPR008993; TNF like.
R InterPro; IPR008993; TNF like.
R PEANTS; PR01234; TNECRSISCT.
R PRINTS; PR01234; TNECRSISCT.
R PRINTS; PR01235; TNF subf; 1.
R PROSITE; PS00271; TNF 11.
R PROSITE; PS00251; TNF 11.
R PROSITE; PS0049; TNF 2; 1.
Chordata; Craniata; Vertebrata; Buteleostomi; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63; Indels 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO; GO:0016020; C:membrane; IEA.
GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 11.2%; Score 144.5; DB 2; Length 216; 1 Similarity 26.9%; Pred. No. 0.00074; 47; Conservative 28; Mismatches 63; Indels 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Qiu L., Song L., Wu L., Cai Z., Xu W., Wang L.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY376595; AAR02413.2; -.
HSSP; P01375; 1A8M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            216 AA; 23793 MW; BADAE3F83F45B533 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                         MEDLINE=98234044; PubMed=9573100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10042;
                                                                                                                                                                                                                                                                                                                                                                                                                         Peromyscus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Signal.
SIGNAL
CHAIN
                                                                                                                                                                                                                                                                                                                   Q80XA4;
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                                                                                                                                                                                                            75 LVRERGPORVAAHITGTRGRSNTLSS---PNSKNEKALGRKINSWESSRSGHSFL-SNLH 130
                                                                                                                                                                                                                          187 SARNSCWSKDAE-----YGLY-SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGA 239
                                                                                                                                                                                                                                                         131 LRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDFI----LLMK 186
                                                                                                                                                                                                                                                                               119 LVNNQIVIPQTGLYFVYCQASFRVSCSNGDEEGAGKGLTPLSHRIWRYSDSIGSKASLVS 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Nutative Tumour necrosis factor alpha two.
Name=TNR-alpha2pro;
Cyprinus carpio (Common carp).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Cyprinus.
NCBI_TAXID=7962;
                                                                                                                                                               Query Match 11.1%; Score 143; DB 2; Length 241; Best Local Similarity 24.3%; Pred. No. 0.0011; Matches 44; Conservative 34; Mismatches 87; Indels 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0016020; C:membrane; IEA.
GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
GO; GO:000555; P:immune response; IEA.
InterPro; IPR006053; TNF Deta.
InterPro; IPR002960; TNF Deta.
InterPro; IPR006963; TNF TMF TMF.
InterPro; IPR008963; TNF TMF TMF.
InterPro; IPR008963; TNF TMF TMF.
InterPro; IPR008963; TNF TMF TMF.
InterPro; IPR008969; TNF TMF TMF.
                                                                                                                              50049; TNF 2; 1.
241 AA; 26702 MW; 2C493CF80651EA2C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                    231 AA
GO; GO:0006955; P:immune response; IEA.
InterPro; IPR005053; TNF abc.
InterPro; IPR002960; TNF beta.
InterPro; IPR006052; TNF lemily.
InterPro; IPR008983; TNF like.
InterPro; IPR008983; TNF like.
InterPro; IPR008983; TNF like.
InterPro; IPR003836; TNF eubf.
PRINTS; PR01234; TNFERZA.
PRODOM; PR01234; TNFERZA.
PRODOM; PR01236; TNF Bubf; 1.
PROSTIE; PS50049; TNF, 2; 1.
PROSTIE; PS50049; TNF, 2; 1.
SEQUENCE 241 AA; 26702 MM; 2C493CF8065
                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PRO1234; TWECROSISFCT.
PRINTS; PRO1234; TWBETA.
ProDom; PD002012; TNF subf; 1.
SMART; SM00207; TNF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
TISSUE=Head kidney;
                                                                                                                                                                                                                                                                                                                                                     240 F 240
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                                                                                                                                                                                                                                                                                                                                                                88 -----YDPDVCKDNL------DWKQNQDQAFVSGGLELVDREIIIPNDGIYFVYSQVSF 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72 ISPLVRERGPQRVAAHITGTRGRSNTL-SSPNSKNEKALGRKINS------WESSRSG 122
                                                                                                                                                                                                                                                                                                                           93 GRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYF 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                   153 RFQEEIKENTKNDKQMV-----QYIYKYTSYPDPILLMKSARNSC-WSKDAEYGLY-S 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56 IGPQREEKFPNNLP--IIGSMAQTLTLRSSSQNSSDKPVAHVVANHQVDEQLEWLSRRAN 113
                                                                                                                                                                                                                                                 44 WQLRQLVRKMILRTSEETISTVQEKQQN-----ISPLVRERGPQRVAAHITGTR
                                                                                                                                                 40; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peromyscus maniculatus (Deer mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Sigmodontinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO; GO:0016020; Cimembrane; IEA.
GO; GO:00164; F:tumor necrosis factor receptor binding; IEA.
GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
GO; GO:0006165; F:tumor nesponse; IEA.
InterPro; IPR006059; TNF abc.
InterPro; IPR006059; TNF family.
InterPro; IPR006098; TNF family.
InterPro; IPR0080983; TNF family.
InterPro; IPR003056; TNF subf.
Pfam; PF00229; TNF: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
10.7%; Score 137.5; DB 2; Length 232;
Best Local Similarity 24.5%; Pred. No. 0.003;
Matches 45; Conservative 36; Mismatches 78; Indels 25
                                                                                   Query Match 11.0%; Score 141; DB 2; Length 231; Best Local Similarity 23.3%; Pred. No. 0.0016; Matches 51; Conservative 38; Mismatches 90; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 20 Potential.
80 >232 tumor necrosis factor.
232 232 AA; 25704 MW; E48A9379DB4F216D CRC64;
PROSITE; PS50049; TNF 2; 1.
SEQUENCE 231 AA; 25927 MW; 2AD8871D0B1A82F1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      204 IYQGGIFELKENDRIFVSVTNEHL--IDMDHEASFFGAF 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        191 IYLGAAFNLRARDRLRTETTKELLPRVESENGKTFFGVF 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Tumor necrosis factor precursor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              232 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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PRINTS; PRO1235; TNFALPHA.
PRODOM; PD002012; TNF subf; 1.
SMART; SM00207; TNF; I.
PROSITE; PS00251; TNF 1; 1.
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NCBI_TaxID=9986;
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                                                                                                61 TISTVQEKQQNISPL---VRERGPQ-----RVAAHITGTRGRSNTLSSPNSKNEKALGRK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              113 INSWESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYI 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            173 YKYT-SYPDPILLMKSARNSCWSKDAEYGLY--SIYQGGIFELKENDRIFVSVTNEHL-- 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  160 MRFSESYGGKKPLFSAIRSICTQEPESENLWYNTIYLGAAPHLREGDRLGTDTTTALLPM 219
123 HSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKY-TSYPDP 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101 TLDWRDDQDQAFSSGGLKLVNREIIIPDDGIYFVYSQVSLHI-SCTSELTEEQVLMSHAV
                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
10.7%; Score 137.5; DB 2; Length 234;
Best Local Similarity 26.4%; Pred. No. 0.0031;
Matches 51; Conservative 30; Mismatches 83; Indels 29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Phelan P.E. III, Mellon M.M., Kim C.H.;
Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY427649; AAR06286.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NF 2; 1.
25826 MW; 6E88DCF46D3F131C CRC64;
                                                                                                                                                                                                                                                                                                                                 05-JUL_2004 (TrEMBLrel. 27, Created)
05-JUL_2004 (TrEMBLrel. 27, Last sequence update)
05-JUL_2004 (TrEMBLrel. 27, Last annotation update)
Tumor necrosis factor.
                                                                                                                                                                                                                                                                                                                                                                                                                 Brachydanio rerio (Zebrafish) (Danio rerio).
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                                                                                                                                                                                                                                                                                               234 AA.
                                                                                                                                                                                                                                                                                               PRT;
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SMART; SM0227; TNF 1.
PROSITE; PS50049; TNF 2; 1.
SEQUENCE 234 AA; 25826 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR01234; TNECROSISFCT.
PRINTS; PR01236; TNFBETA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           220 VENDNGKTFFGVF 232
                                                                                                                                                                                                                                                                                               PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00229; TNF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P01375; 1A8M.
                                                                                                                                                       236 -FFG 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                              228 VYFG 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=7955;
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ID TNFA RABIT
AC P04924;
                                                                           182
                                                                                                                                                                                                                                                                                               Q6T9C7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Molecular cloning and expression in Escherichia coli of the CDNA coding for rabbit tumor necrosis factor.";

In DNA 5:149-156(1986).

Coding for rabbit tumor necrosis factor.";

In DNA 5:149-156(1986).

Color State of the that binds to TNFRSFIA/TNFR1 and TNFRSFIB/TNFRE. It is mainly secreted by macrophages and can induce cell death of certain tumor cell lines. It is potent pyrogen causing fever by direct action or by stimulation of interleukin 1 secretion and is implicated in the induction of cachexia, Under certain conditions it can stimulate cell proliferation and induce cell differentiation.

Color SUBURITH Hondortimer (By similarity).

Color SUBURITH CACATION: Type II membrane protein. Also exists as an extracellular soluble form (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               similarity).
DISEASE: Cachexia accompanies a variety of diseases, including
cancer and infection, and is characterized by general ill health
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDILINE-86219711, PubMed=3519137,
Ito H., Yamamoto S., Kuroda S., Sakamoto H., Kajihara J., Kiyota T.,
Hayashi H., Kato M., Seko M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDILNE-21055334; Pubmed=2249779; DOI=10.1016/0378-1119(90)90364-W;
Shakhov A.N., Kuprash D.V., Azizov M.M., Jongeneel C.V.,
Nedospasov S.A.;
13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
Tumor necrosis factor precursor (TNP-alpha) (Tumor necrosis factor precursor (TNP-alpha) (Tumor necrosis factor Name=TNFA) (TNF-a) (Cachectin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           proteolytic processing (By similarity).

PTM: The membrane form, but not the soluble form, is phosphorylated on serine residues. Dephosphorylation of the membrane form ocurrs by binding to soluble TNFRSFIA/TNFRI (By
                                                                                                                                                                                                                                                                                                     Eukaryotā; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ito H., Shirai T., Yamamoto S., Akira M., Kawahara S., Todd C.W.,
Wallace R.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Structural analysis of the rabbit TNF locus, containing the encoding TNF-beta (lymphotoxin) and TNF-alpha (tumor necrosis factor).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'Molecular cloning of the gene encoding rabbit tumor necrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: Belongs to the tumor necrosis factor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WEDLINE=86219712; PubMed=3519138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPRO06053; TNF abc.
InterPro; IPRO06052; TNF family.
InterPro; IPRO08983; TNF_like.
InterPro; IPR003636; TNF_subf.
                                                                                                                                                                                                                                                        Oryctolagus cuniculus (Rabbit)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M12845; AAA31486.1; -.
EMBL; M12846; AAA31482.1; -.
EMBL; M60340; AAA31484.1; -.
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HSSP; P06804; 2TNF.
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Tumor necrosis factor, membrane form.
Tumor necrosis factor, membrane form.
Tumor necrosis factor, soluble form.
Cytoplasmic (Potential).
Signal-anchor for type II membrane
protein (Potential).
Extracellular (Potential).
Cleavage (by ADAMI7) (By similarity).
Phosphoserine (by CK1) (By similarity).
By similarity.
Missing (in Ref. 3).
                                                                                                                                                                                                                                                                                                                      Query Match 10.6%; Score 136.5; DB 1; Length 235; Best Local Similarity 23.0%; Pred. No. 0.0037; Matches 42; Conservative 37; Mismatches 81; Indels 23.
            PRINTS; PRO1234; TNECROSISFCT.
ProDom; PD002012; TNF subf; 1.
PROSTIE; SM00207; TNF; 1.
PROSTIE; PS50049; TNF 1; 1.
PROSITE; PS50049; TNF 2; 1.
Cytokine; Phosphorylation; Signal-anchor; Transmembrane.
CHAIN 1 235 Tumor necrosis factor, memborane 1 235 Tumor necrosis factor, solub DOMAIN 1 35 Cytoplasmic (Potential).
TRANSMEM 36 56 Signal-anchor for type II memborane.
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Amino aci Protein f Protein f Protein f

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The present invention provides one kind of mutant 95-281 recombinant soluble polypeptide (rsTRAILthr95gly-281) in human TRAII extracellular region. The preparation process and antineoplastic application of the recombinant soluble polypeptide are also provided. The present sequence represents human TRAI-1 extracellular region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEETISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New tumor necrosis factor relative cell death inducing ligand extracellular region mutation polypeptide, used for an antineoplastic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         extracellular region; antineoplastic.
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ABG80597
ADJ82119
AAB67248
ADJ82134
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AAB08273
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ADJ82116
                                                                                                                                                                                                                                                                         ADJ82133
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                                                                                                                                                                                                                                                                                                                                                                                        ADN35127 standard; protein; 187 AA
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WPI; 2004-023846/03.
Sequence 187 AA;
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                                                                                                                                                                                                                   122 YPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFF 181
                                                                                         SSRSGHSFLSNLHLRNEGLVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTS 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WESSRSGHSFLSNLHLRNGELVIHKEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYK 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to a cell factor derivative (TRAILD) used as an anticancer derivative. The TRAIL protein can be expressed in soluble form in bacterial cytoplasm. The present sequence represents a TRAILD amino acid sequence. Recombinant TRAILD fusion proteins can be used in anti-cancer medicaments to treat cancer of the liver, breast, or kidney. It can also be used to treat leukaemia
2 SEETISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWE 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New cell factor derivative causing cells to die, for anticancer therapy.
                                                         SSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTS
                                                                                                                                                                                YPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RTSEETISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cell factor derivative; TRAILD; anticancer; cancer; liver; breast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cell factor derivative TRAILD amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BASI-) INST BASIC MEDICAL SCI CHINESE ACAD MEDI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY88630 standard; protein; 220 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 2; 10pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99CN-00111039
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-351201/31.
                                                                                                                                                                                                                                                                                                      GAFLVG 243
                                                                                                                                                                                                                                                                                                                                                                GAFLVG 187
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les 185; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          kidney; leukaemia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-JUL-1999;
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                                                                                                                   62
                                                                                                                                                                                178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zheng D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              131 LRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQXIYKYTSYPDPILLMKSARN 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 LRNGELVIHEKGFYYIYSQTYFRFQEEIKENAKNDKQWVQYIYKYTSYPDPILLMKSARN 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71 NISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 SCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tumor death induction ligand gene, gene expression protein and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                  Human, tumour related apoptosis inducing ligand, Trail109, Trail prokaryotic expression system; tumour cell death.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
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Pred. No. 2.7e-80;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 7; Page 10 (disclosure); 17pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TWOM-) NO 2 MILITARY MEDICAL COLLEGE PLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Encoded by CTT"
                                                                                                                                                                                       Partial human Trail protein, Trail109
                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
ABG72258 standard; protein; 173 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-NOV-2001; 2001CN-00132371.
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                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        preparation method
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YTSYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEA

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TRAIL; TNF receptor apoptosis including ligand; human; SDR5;
tumour necrosis factor; crystal structure; TRAIL-SDR5 complex; apoptosis.
                                                                                                            10-JAN-2001; 2001WO-KR000034.
                                                                                                                                  29-DEC-2000; 2000KR-00085947.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                              WPI; 2002-583613/62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 168 AA;
                                                                WO200253727-A1.
                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     961
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                                                                                                                                                      (DONG-) I
(UYPO-) I
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Matches
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ID ABG7
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AC ABG7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        136 LVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDFILLMKSARNSCWSK 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                 Human; TRAIL; tumour necrosis factor; TNF;
tumour necrosis factor related apoptosis inducing ligand; TRAIL; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Factor (TNF) Related Apoptosis Inducing Ligand (TRAIL) protein, and for crystallising the TRAIL protein and its three-dimensional structure, where the TRAIL protein has improved activity, which specifically kills cancer cells and cells infected by virus. The present sequence is human TRAIL, which was used in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to a method for producing Tumour Necrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 VRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                      Producing and crystallizing tumor necrosis factor related apoptosis inducing ligand protein, and its three-dimensional structure.
                                                                                                                                                                                                                                                                                                                   Yoon SJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     196 DAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human TNF related apoptosis including ligand (TRAIL) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68.9%; Score 887; DB 4; Length 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                  Yoon JI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Pred. No. 2.3e-78; cive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                  oh BH,
                                                                                                                                                                                                                                                                                                                 Lim GM,
                                          ABB76826 standard; protein; 168 AA
                                                                                                                                                                                                                                                                                            (DONG-) DONG WHA PHARM IND CO LTD
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                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 14; 20pp; Korean.
                                                                                                                                                                                                                                                99KR-00035354.
                                                                                                                                                                                                                                                                     99KR-00035354.
                                                                                                                                                       viral infection; cytostatic.
                                                                                                                                                                                                                                                                                                                  Kim JU, Lee GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-OCT-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 68.9
Best Local Similarity 100.
Matches 168; Conservative
                                                                                                                                                                                                                                                                                                                                      WPI; 2001-533833/59.
                                                                                                                                                                                                                                                                                                                                                  N-PSDB; ABL53366.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 168 AA;
                                                                                                                                                                                                   KR2001019100-A
                                                                                                                                                                                                                                                                     25-AUG-1999;
                                                                                                                                                                              Homo sapiens
                                                                                      16-JUL-2002
                                                                                                            Human TRAIL
                                                                                                                                                                                                                         15-MAR-2001
                                                                ABB76826;
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TD AAU9
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This invention relates to an expression vector containing the tumour necrosis factor related apoptosis inducing ligand (TRAIL) protein receptor TSTS. The invention also comprises a method for producing the some special from an E. coli transformed with the vector. The method of the invention is useful for crystallising the TRAIL-SDRS complex. A TRAIL-SDRS crystal complex is useful for developing recombinant proteins i.e. proteins with improved stability or cytotoxic activity of a TRAIL protein which involves changing the amino acid of the AA loop to increase the various interactions between amino acid of the AA loop to increase the various interactions between amino acids of from the binding site of metal ions or the disulfide bonding, or changing the corresponding amino acids of the homotrimer interface or homodimer interface to increase the various interactions between amino acids or from the binding site of metal ion or disulfide bond, or to fill the cavity. A 3 dimensional conferring specificity for the recognition between TNP family members and for the development of TRAIL protein, which has a better stable, cytotoxic activity or an improved receptor binding affinity. The present sequence represents the human tumour necrosis factor receptor apoptosis including ligand (TRAIL) protein sequence used in the invention
                                                                                                                                                                                                                                                                                                               Novel expression vector containing an sDR5 encoding gene transformed into Escherichia coli to produce sDR5 protein for crystallizing a tumor necrosis factor-related apoptosis-inducing ligand-sDR5 complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         136 LVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSK 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 LVIHEKGFYYIYSQTYFRFQEEIKENTKONDKQMVQYIYKYTSYPDFILLMKSARNSCWSK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 VRERGEORVAAAHITGTRGRSNTLSSPNSKONEKALGRKINSWESSRSGHSFLSNLHLRNGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 168
                                                                                                                                     Cha
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100.0%; Pred. No. 2.3e-78;
ive 0; Mismatches 0;
                                                                                                                                     Lim KM,
                                                                                                                                     Chung YH, Ryu JM, Hwang YH, Yoon JI,
DONG WHA PHARM IND CO LTD.
UNIV POHANG SCI & TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABG72259 standard; protein; 168 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 5; Page 70; 74pp; English.
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Unidentified
                                                                                                                                                                                                                                                        Novel pol
proteins,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABR84402;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
                                                                                                                                                                                                                                                                                                                                                                The present invention relates to the isolation of CDNA encoding human tumour related apoptosis inducing ligand (Trail), and the Trail protein. The Trail full length CDNA is cloned, and is utilised to create a Trail prokaryotic expression system. The full length Trail cDNA is used to respectively clone cDNA of soluble ectocytic segment Trail109 and Trail 14, and respectively create Trail109 cDNA and Trail1109 and Trail expression systems. The prokaryotic expression systems created greatly increase the expression and quantity of the Trail, Trail109, and Trail114 proteins, and may be useful in a new preparation for killing tumour realls. The present sequence represents the partial human Trail protein, trail114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSK 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 LVIHEKGFYYIYSQTYFRFQEEIKENAKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VRERGEORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                               Tumor death induction ligand gene, gene expression protein and its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 882; DB 5; Length 168;
Pred. No. 7.2e-78;
0; Mismatches 1; Indels
                                          Human, tumour related apoptosis inducing ligand, Traill14,
Trail prokaryotic expression system, tumour cell death.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DAEYGLYSIYQGGIPELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Amino acid sequence of a human TNF ligand TRAIL.
                                                                                                                                                                                                                                                                                                                                               Claim 7; Page 10 (disclosure); 17pp; Chinese.
                                                                                                                                                                                                                                   (TWOM-) NO 2 MILITARY MEDICAL COLLEGE PLA.
                                                                                                                       /note= "Encoded by CTT"
                       Trail114
                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB08274 standard; protein; 166
                    Partial human Trail protein,
                                                                                                                                                                                       30-NOV-2001; 2001CN-00132371.
                                                                                                                                                                                                             30-NOV-2001; 2001CN-00132371.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 68.5%;
Best Local Similarity 99.4%;
Matches 167; Conservative (
(first entry)
                                                                                                                                                                                                                                                                             WPI; 2002-751439/82.
                                                                                                           Misc-difference 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                        preparation method
                                                                                                                                                                                                                                                                                          N-PSDB; ABX14393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 168 AA;
                                                                                                                                                                                                                                                         Yao Y;
                                                                             Homo sapiens
04-MAR-2003
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                                                                                                                                           CN1354183-A
                                                                                                                                                                   19-JUN-2002
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                                                                                                                                                                                                                                                        Hu Y,
셤
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61 IHEKGFYYIYSQTYFRFQEEIKENTKNDKQWVQYIYKYTSYPDPILLMKSARNSCWSKDA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB08265-83 represent tumour necrosis factor (TNF) ligands. The specification describes an AGP-3 polypeptide, which is TNF ligand family member. AGP-3 is a type II transmembrane protein, and is a potent B cell stimulatory factor. Expression of AGP-3 correlates to increases in the number of B cells and immunoglobulins produced. AGP-3 proteins, and nucleic acids may be used to treat inflammatory and immune disorders, e.g. rheumatorid arthritis, Crohn's disease, lupus and graft versus host disease. The nucleic acids may be used to regulate the expression of an AGP-3 related protein. The AGP-3 proteins, antibodies and nucleic ands are also useful for the detection of AGP-3 agonists, antagonists and characterizing interactions with AGP-3 related proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78 ERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polypeptides comprising tumor necrosis factor ligand family ins, useful for treating inflammatory and immune disorders, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
AGP-3; tumour necrosis factor ligand; TNF ligand; Crohn's disease; type II transmembrane protein; B cell stimulatory factor; inflammatory disorder; immune disorder; rheumatorid arthritis; lupus and graft versus host disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68.2%; Score 878; DB 3; I
100.0%; Pred. No. 1.7e-77;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Š
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 14; Fig 9; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0119906P.
99US-0166271P.
                                                                                                                                                                                                                                                                                                                                                                                        11-FEB-2000; 2000WO-US003653.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 100.
Les 166; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-558217/51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 166 AA;
                                                                                                                                                                                                                                                  40200047740-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (AMGE-) AMGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-FEB-1999;
18-NOV-1999;
                                                                                                                                                                                    domo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-OCT-2003
                                                                                                                                                                                                                                                                                                                       17-AUG-2000
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12. .44
'label=
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 161 AA;
                                                                                                                                                                                            WO200068378-A1
                                                                                                                                                                                                               16-NOV-2000
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                                                                                                                                                             Region
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                                                                                                                                                                                                                                                                                                                              1;
                                                                                                                                                                                                                        The invention relates to a TNF-related apoptosis-inducing ligand encoding (TRAIL) cDNA and its encoded polypeptide. The gene of the invention is related to mutational human tumour necrosin. The polypeptide of the invention is useful for inducing the death of tumour cells. The current sequence represents the TRAIL amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                      ELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQWVQYIYKYTSYPDPILLMKSARNSCWS 118
                                                                                                                                                                                                                                                                                                                                                  75 LVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNG 134
                                                                                                                                                                                                                                                                                                                                                                                        ELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWS 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    haemolytic anaemia; Grave's disease; myasthenia gravis; TRAIL protein; post-streptococcal glomerulonephritis; polyarteritis nodosa; BCMA; B cell maturation factor; pemphigus vulgaris; B-lymphocyte proliferation.
                                                                                                                                                                                                                                                                                                                                                            Human; Tumour Necrosis Factor; TNF; immunosuppressant; TALL-1;
Tumour necrosis factor and Apol.related Leucocyte expressed Ligand 1;
therapy; autoimmune disorder; rheumatoid arthritis; multiple scleris;
systemic luque erythematosus; SLE; insulin dependent diabetes mellitus;
thrombocytopenia purgura; acute rheumatic fever; Goodpasture's syndrome;
                                                                                                                                                           Death induced ligand (TRAIL) cDNA and encoded polypeptide, useful for inducing the death of tumor cells, is related to mutational human tumor
                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                              7
                                                                                                                                                                                                                                                                                                                                                                                                                                KDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 243
                                                                                                                                                                                                                                                                                                                                                                                                                                          67.3%; Score 866; DB 6; Length 167; 98.2%; Pred. No. 2.6e-76; Live 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C-terminal region of human TRAIL protein.
                                                                                        (CHEN-) CHENGDU DIAO PHARM GROUP CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2. .8
/label= Beta_strand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32. .34
/label= Beta_strand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY71985 standard; protein; 161 AA
                                                                                                                                                                                                     Claim 4; Fig 2; 14pp; Chinese.
                                                 10-APR-2001; 2001CN-00105946.
                                                                    10-APR-2001; 2001CN-00105946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                            Gao X, Liu Z;
                                                                                                                                2003-230973/23.
                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                          N-PSDB; ACC83357
                                                                                                                                                                                                                                                                                     Sequence 167 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-MAR-2001
         CN1380339-A
                                                                                                                                                                                                                                                                                                                    Best Local Sim:
Matches 166;
                             20-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                         135
                                                                                                                                                                                                                                                                                                                                                                                                                                195
                                                                                                                                                                                                                                                                                                                                                                                                                                                  119
                                                                                                                                                                                   necrosin.
                                                                                                                                                                                                                                                                                                                                                                                                            29
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                                                                                                                                                                                                                                                                                                         Query Match
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Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Region
                                                                                                            Li B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 9
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The present invention relates to Tumour necrosis factor (TNF) and Apolrelated Leucocyte expressed Ligand 1 (TALL-1) nucleic acid molecules, proteins including homologues), and their antibodes. The invention in particular relates to methods for regulating the interaction between TALL-1 and TALL-1 receptors (BCMA referred as B cell maturation factor) to regulate monocyte, macrophage and B lymphocyte mediated immune responses. TALL-1 protein is useful for identifying compunds that regulate B lymphocyte proliferation. It is also useful for treating B lymphocyte associated autoimmune disorders like rheumatoid arthritis, systemic lupus erythematosus (SLB), insulin dependent diabetes mellitus, multiple sclerosis, myasthenia gravis, Grave's disease, autoimmune haemolytic anaemia, autoimmune thrombocytopenia purpura, Goodpasture's syndrome,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pemphigus vulgaris, acute rheumatic fever, post-streptococcal glomerulonephritis, or polyarteritis nodosa. The TALL-1 protein and its corresponding nucleic acid sequence are also useful in diagnostic assays. The present sequence is a C-terminal region of human TRAIL protein. which has 20-25% sequence identity with the C-terminal region of human TALL-1 protein extracellular domain. TRAIL protein is a TNP family member
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated TALL-1 protein is used to identify compounds that regulate lymphocyte proliferation, used to treat B lymphocyte associated autoimmune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
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                      77. .50
|Tabel= Beta_strand
                                                                                                                                                      61. .72
/label= Beta_strand
                                                                                                                                                                                                                 86. .91
/label= Beta_strand
                                                                                                                                                                                                                                                                                                                                       18. .128
|abel= Beta_strand
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/label= Beta_strand
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-MAY-1999; 99US-0132892P.
01-MAY-2000; 2000US-0201012P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35-MAY-2000; 2000WO-US012266
                                                                                                                                                                                                                                                                               99. .109
/label= B
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Matches 161; Conservative
                                                                                           53. .56
/label= 1
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ADC03335 standard; protein; 161 AA.
                                                                                          18-DEC-2003
                                                                                                                                                                                                                                13-MAR-2003.
                                                                    ADC03335;
                                                                                                                                                                                                                                                                                                                                   (NELS/)
(FREM/)
                                                                                                                                                                                                                                                                                                            (ROSS/)
                                                                                                                                                                                                                                                                                                 LAMJ/)
                                                                                                                                                                                     Mus sp.
                                                                                                                                                                                                                                                                                                                                                                     Lam J,
                                                                                                                                                              TRAIL.
                      RESULT 11
ADC03335
                                                          The invention relates to a composition (I) comprising a protein complex in crystalline form, where the complex comprises an amino acid sequence of a Receptor Activator of Necrosis Factor KB (RANK) Ligand (RANKL) ectodomain. (I) is useful for identifying a compound with RANK modulating activity, and for identifying a RANK or OPG modulating compound. (I) is useful to intelligently design mutants that have altered biological properties and for identifying mutants that have altered biological properties and for identifying new therapeutic agents. (I) is also useful to computationally screen small molecule databases for chemical entities or compounds that can bind in whole, or in part, to RANK or RANKL. The present sequence respresents a tumour necrosis factor (TNF) family member, TRAIL (164v), used in a structural-based alignment study
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  142
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                                                                                                                                                                                                                                                                                                                                                                                                    Composition for identifying a compound with Receptor Activator of Necrosis Factor kB, RANK modulating activity and for identifying RANK or osteoprotegerin modulating compound, has a protein complex in crystalline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDFILLMKSARNSCWSKDAEYGLY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDFILLMKSARNSCWSKDAEYGLY
                                                                                                                                                                       RANK; receptor activator of necrosis factor kB; RANK ligand; RANKL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 161;
                                                                                                                                                                                                                                                                                                                                                          Fremont DH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 243
             SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66.0%; Score 850; DB 6; Le
ion 0%; Pred. No. 9.2e-75;
                                                                                                                                                INF family member, TRAIL (1d4v) protein fragment.
                                                                                                                                                                                    tumour necrosis factor; TNF; TRAIL; cytokine.
                                                                                                                                                                                                                                                                                                                                                          Teitelbaum SL, Nelson CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Prec. ....
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure, Fig 3, 66pp, English.
                                                                               ABR39855 standard; protein; 161
                                                                                                                                                                                                                                                                                                                                    (BARN-) BARNES-JEWISH HOSPITAL
                                                                                                                                                                                                                                                                            09-AUG-2002; 2002WO-US025287.
                                                                                                                                                                                                                                                                                                 09-AUG-2001; 2001US-0311163P. 22-MAR-2002; 2002US-00105057.
                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      murine RANKL protein
                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-256526/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
Les 161; Conserv
                                                                                                                                                                                                                                                                                                                                                          Ross FP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 161 AA;
                                                                                                                                                                                                                               WO2003014077-A2
                                                                                                                                                                                                         Unidentified
                                                                                                                           11-AUG-2003
                                                                                                                                                                                                                                                     20-FEB-2003
  203
                      121
                                                                                                      ABR39855;
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                                                                                                                                                                                                                                                                                                                                                          Lam J,
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Matches
                                                         RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
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The invention relates to a composition comprising a protein complex in crystalline form, where the complex comprises an amino acid sequence of a receptor activator of nuclear factor kappaB (NPKappaB) (RANK) ligand (RANKL) ectodomain. The three-dimensional structural representation of a RANKL ectodomain crystal complex, is useful for identifying a RANK or osteoprotegarin (OPG) modulating compound, and for identifying a Compound with RANK modulating activity. The crystals permit the determination of the three-dimensional X-ray diffraction structure of the crystal-line polypeptide to high resolution. The atomic structure coordinates and structural information which comprises atomic structure coordinates and structures for solving the three-dimensional X-ray diffraction the coordinates for solving the three-dimensional X-ray diffraction of and/or solution. The structural information may also be used in a variety of molecular modeling and computer-based screening applications to, for example design mutants of the crystallized RANKL, its receptors, or a portion or fragment of RANKL or its receptors. The coordinates of such structural coordinates of the RANKL crystal, crystal, or subsets of such structural coordinates of the RANKL crystal, crystal, or subsets of such structural coordinates of the RANKL crystal, crystal, or subsets of dentifying candidate compounds capbable of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Composition comprising crystalline receptor activator of NFkappaB (RANK) ligand ectodomain complex whose three-dimensional structural representation is useful for identifying RANK or osteoprotegrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         modulating RANK biological activity, and for identifying compounds which mimic the capability of RANKL to bind RANK molecules, thereby activating the receptor. The present sequence represents the amino acid sequence of the tumour necrosis factor family cytokine, TRAIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                         RANKL ectodomain crystal complex; RANK; osteoprotegerin; OPG; bone-forming compound; tumour necrosis factor; TNF family; cytokine;
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                                                                                       Tumour necrosis factor family cytokine, TRAIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nelson CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Teitelbaum SL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure, Fig 3; 40pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-AUG-2002; 2002US-00215446.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-AUG-2001; 2001US-0311163P.
(first entry)
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TEITELBAUM S L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NELSON C A.
FREMONT D H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-605763/57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 modulating compound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ross FP,
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19-JUN-2003
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                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X2XHXHXBXBXBXBXXXHLLLXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention discloses isolated, naturally occurring, polypeptide splice variants of human tumour necrosis factor (TNF)-related apoptosis inducing ligand (TRALL). Apoptosis, or programmed cell death, occurs during normal cellular differentiation and development of multicellular organisms. Apoptosis is induced by certain cytokines which include TNF and TRALL distormed for as Apo-2 ligand, Apo-2L). TRALL is a type II membrane protein which induces apoptosis and nuclear factor-B (NF-B) activation in many tissues and cells. Receptors for TRALL include two death domain
                                                         61 FYYIYSQIYFRFQEEIKENTKNDKQMVQYIYKYTSYPDFILLMKSARNSCWSKDAEYGLY 120
RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 142
                                              202
           New splice variants of tumor necrosis factor-related apoptosis inducing ligand (TRAIL) isolated from B-lymphocytes and liver, useful to treat diseases or disorders associated with low expression of the variants.
                                                                                                                                                                                                                                                          Human; cytostatic; neuroprotective; immunosuppressive; splice variant; tumour necrosis factor; TNF; TNF-related apoptosis inducing ligand; TRAIL; apoptosis; programmed cell death; differentiation; development; cytokine; Apo-2 ligand; Apo-21; nuclear factor-B; NF-B; type I interferon; tumour; antitumour; gene therapy; cytotoxic; cancer; therapeutic; neurodegenerative disease; autoimmune disease; aging;
                                             PYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Encoded by in-frame stop codon"
                                                                                        203 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 243
                                                                                                     SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 161
                                                                                                                                                                                                                                     Human TRAIL splice variant 8, rpl-6-6, protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                        'note= "Extracellular domain"
                                                                                                                                                                                                                                                                                                                                                                                                                     "Transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                               "Cytoplasmic domain"
                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                   AAU99301 standard; protein; 212 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-MAY-2001; 2001US-00855544.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-MAY-2000; 2000IL-00136156
                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                               chromosome 3q26; rp1-6-6.
                                                                                                                                                                                                                                                                                                                                                                                                                               .212
                                                                                                                                                                                                                                                                                                                                                                                                           .38
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/note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Khosravi R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-479259/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (YBLI/) YBLIN R.
(KHOS/) KHOSRAVI R.
(SAVI/) SAVITZKY K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference
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                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                24-SEP-2002
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  83
                                             143
                                                                                                             121
                                                                                                                                                                                          AAU99301;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         felin R,
                                                                                                                                                                                                                                                                                                                                                                                    Domain
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containing receptors, DR4 and DR5, as well as two decoy receptors, DCR1 and DCR2, lacking the intracellular signalling death domain. TRAIL, induced by type I interferons, induces apoptosis in tumour cells, whereas normal cells are relatively resistant without showing significant toxic side effects. Thus, TRAIL has the potential to be a very useful antitumour agent. The naturally occurring splice variants may differ in their cellular distribution, expression levels/timing and activity. Determining these factors could provide possible mechanisms for the induction of apoptosis of tumours cells. The splice variant polypeptides and polymucleotides can be used in gene therapy, to raise antibodies, to detect the levels, distribution and ratios of expression of TRAIL, and its splice variant TRAIL products and modulate its activity (agonists which bind the variant TRAIL products and modulate its activity (agonists and antagonists). Pharmaceutical compositions, comprising an expression vector or any of the amino acid sequences, are useful for causing a cytotoxic effect in cancer cells and for treatment of diseases which can be ameliorated, cured or prevented by lowering or raising the level of the amino acid sequences, are useful for causing the the amino acid sequences, are useful for causing a cytotoxic effect in cancer cells and for treatment of diseases which variant thity in blocking or decreasing the activity of the TRAIL variant cultility in blocking or decreasing include cancer, neurodegenerative accounts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diseases, autoimmune diseases, diseases involved in the non-normal development of tissues and aging. TRAIL's gene is located on chromosome 1326. The sequence presented is the human TNP-related apoptosis inducing ligand (TRAIL) splice variant 8, rpl-6-6, protein which has had an C-terminal section of the conserved TNP domain deleted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39 TNELKOMODKYSKSGIACFLKEDDSYWDPNDEESMNSPCWOVKWOLROLVRKMILRTSEE 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TNELKOMODKYSKSGIACFLKEDDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antirheumatic; antiarthritic; neuroprotective; antiinflammatory; antidiabetic; dermatcological; antiasthmatic; neutroxine-alpha; crystallography, cancer, allergic disorder; autoimmune disease; rheumatoid arthritis; multiple sclerosis; Crohn's disease; diabetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SCHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQKKKKKTSVSTCYFFQXNY 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIY 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10; Indels
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Pred. No. 2.4e-72;
5; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              systemic lupus erythematosus; asthma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADI53053 standard; protein; 154 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human TRAIL protein (aa 119-281).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          figure sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64.3%;
91.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 212 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO2003050134-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-APR-2004
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(PFIZ ) PFIZER PROD INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               193
                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                           Cai JH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AD02477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                    The invention relates to a neutrokine-alpha protein in crystalline form. The crystalline neutrokine-alpha protein is useful for designing molecules that have biological activity or compounds that bind, inhibit or minic a neutrokine-alpha protein and/or enhance the activity of a neutrokine-alpha protein. The three-dimensional structure of a neutrokine-alpha protein. The three-dimensional structure of a neutrokine-alpha protein and their homologs. The compounds that minic, prevent or inhibit the activity of the protein are useful for treating cancer, allergic disorders, or autoimmune diseases such as rheumatoid arthritis, multiple sclenosis, Crohn's disease, diabetes, systemic lupus erythematosus or asthma. This sequence represents the human TRAIL protein amino acids 119-281 which is used in the invention for comparison to the
                                                                                                                                                                                                                                                                                                                                                                                                                           1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cytostatic; dermatological; antirheumatic; antiarthritic;
neuroprotective; canine; feline; TNF-related apoptosis-inducing ligand;
TRAIL; apoptosis; cancer; neurodegenerative disease; lupus erythematosus;
rheumatoid arthritis; multiple solerosis; diagnosis; genetic testing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  PQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHE 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KGFYYIYSQTYFRQEEIKENTKNQKQMVQYIYKYTXXXXPILLLMKSARNSCWSKDAEYG 111
                                                                                                             New crystalline Neutrokine-alpha protein, useful for designing compounds that bind, inhibit or mimic a Neutrokine-alpha protein or enhance the activity of a Neutrokine-alpha protein for treating e.g. cancer or allergic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYG 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51
                                                                                                                                                                                                                                                                                                                                                                                                                                                              9; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                Score 764.5; DB 7; Length 154;
Pred. No. 2e-66;
0; Mismatches 6; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          201 LYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 243
                                                                                                                                                                                                                                                                                                                                                  numan neutrokine-alpha protein (ADI53050).
                                                                       Arnold E, Volovik Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADO24774 standard; protein; 171 AA
                                                                                                                                                                                 Disclosure, Fig 1, 362pp; English
 07-NOV-2002; 2002WO-US035661.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-OCT-2003; 2003WO-IB004635.
                       07-NOV-2001; 2001US-0331049P.
                                                                                                                                                                                                                                                                                                                                                                                                   59.4%;
                                               (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cat soluble TRAIL protein
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 59.4
Best Local Similarity 90.8
Matches 148; Conservative
                                                                                             WPI; 2003-532895/50.
                                                                       Oren DE,
                                                                                                                                                                                                                                                                                                                                                                           Sequence 154 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO2004039307-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               141
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                                                                       Li Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 1
ADO24774
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 ELVIHQREYYIYSQTYFRFQEPEETEQNRKRNKQMVQYIYKYTSYPDPILLMKSARNSC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cytostatic; dermatological; antirheumatic; antiarthritic;
neuroprotective; canine; feline; TNF-related apoptosis-inducing ligand;
TRAIL; apoptosis; cancer; neurodegenerative disease; lupus erythematosus;
rheumatoid arthritis; multiple sclerosis; diagnosis; genetic testing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated polypeptide (I) comprising a canine or feline TNF-related apoptosis-inducing ligand (TRAIL) sequence and optionally a fusion peptide fused to the polypeptide. Modulators of (I) are useful for treating an apoptosis-related disorder in a subject. The apoptosis-related disorder is chosen from cancer, neurodegenerative disease, lupus erythematosus, rheumatoid arthritis and multiple sclerosis. (I) is useful for diagnostic evaluation, genetic testing and/or prognosis of angiogenesis-related disorders, such as cancer. This sequence represents a gene encoding a cat soluble TRAIL protein used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                  Novel isolated canine or feline TNF-related apoptosis-inducing ligand polypeptide, useful for diagnostic evaluation, genetic testing and/or prognosis of angiogenesis-related disorders, such as cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75 LVRERGPORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 WSKDSEYGLYSIYQGGIFELKENDRIFVSVSNEQLIDMDQEASFFGAFLIG 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cat soluble TRAIL with a C-terminal V5-His tag protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59.4%; Score 764; DB 8;
84.2%; Pred. No. 2.6e-66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 29; 151pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AD024776 standard; protein; 201 AA
30-OCT-2002; 2002US-0422342P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-OCT-2002; 2002US-0422342P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 144; Conservative
                                                               (PFIZ ) PFIZER PROD INC.
                                                                                                                                                                                                                WPI; 2004-376043/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                              N-PSDB; AD024773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 171 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the invention.
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XX
WPI; 2004-376043/35.

DR N-PSDB; AD024775.
XX
Novel isolated canine or feline TNF-related apoptosis-inducing ligand polypeptide, useful for diagnostic evaluation, genetic testing and/or prognosis of angiogenesis-related disorders, such as cancer.
XX
Disclosure; SEQ ID NO 31; 151pp; English.
XX
CC
The invention relates to an isolated polypeptide (I) comprising a canine or feline TNF-related apoptosis-inducing ligand (TRAL) sequence and optionally a fusion peptide fused to the polypeptide. Modulators of (I) are useful for treating an apoptosis-related disorder in subject. The apoptosis-related disorder is chosen from cancer, neurodegenerative clasease, lupus erythematosus, rheumatoid arthritis and multiple classes. In useful for diagnostic evaluation, generic testing sequence represents a gene encoding a cat TRALL protein with a V5-His Tag XX
Squence 201 AA;
Squence 201 AA;
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Search completed: June 3, 2005, 06:40:57 Job time: 164 Bec8

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3, 2005, 06:44:02; Search time 139 Seconds (without alignments) 604.318 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                 US-10-662-431-2_COPY_39_281
1287
1 TNELKQMQDKYSKSGIACFL.....NEHLIDMDHEASFFGAFLVG 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Published Applications AA:*

| cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB_pep:*
3: /cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
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6: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
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19: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1465611 segs, 345679903 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                  OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 243
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                                                                                                                                                                                                                           June
                                                                                                                                                                                                                                                                                                                                                                                                                              Perfect score:
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                                                                                                                                                                                                                               Run on:
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SUMMARIES

	Description	Sequence 4, Appli	Sequence 10, Appl	Sequence 14, Appl	æ	Sequence 29, Appl	Sequence 29, Appl	Sequence 7, Appli	Sequence 11, Appl	Sequence 11, Appl	Sequence 11, Appl	Sequence 10, Appl	Sequence 16, Appl	Sequence 14, Appl
	ID	US-10-855-559-4	US-09-900-530A-10	US-10-981-989-14	US-09-779-050A-16	US-10-116-378-29	US-10-959-537-29	US-10-216-074-7	US-10-338-083-11	US-10-611-399-11	US-10-794-751-11	US-10-778-890-10	US-09-855-544A-16	US-09-855-544A-14
	03	17	σ	17	0	13	17	14	14	16	17	17	σ	σ
	Query Match Length DB ID	228	168	168	166	164	164	191	161	161	161	158	208	188
#º	Query Match	69.3	68.9	68.9	68.2	66.7	66.7	66.0	66.0	0.99	0.99	64.9	64.2	58.0
	Score	892.5	887	887	878	859	859	850	849	849	849	835	826	746.5
,	Rebult No.		7	m	4	2	9	7	80	6	10	11	12	13

PINSKNEKALGRKINSWESSRSGHSFLSNIHLIRNGELVIHEKGFYYIYSQTYFRFQEEIKE 145

PNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKE 160

101 98

유 상 A

8

85

52 KMILRISEETISTVQEKQQNISPL------VRERGPQRVAAHITGTRGRSNTLSS 100

Sequence 17, Appl Sequence 12, Appl Sequence 10, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 21, Appl Sequence 22, Appli Sequence 22, Appli Sequence 24, Appli Sequence 10, Appl Sequence 11, Appl Sequence 11, Appl Sequence 12, Appl Sequence 13, Appl Sequence 13, Appl Sequence 13, Appl Sequence 14, Appl Sequence 15, Appl Sequence 15, Appl Sequence 23, Appl Sequence 32, Appl Sequence 320, Appl Sequence 320, Appl Sequence 320, Appl Sequence 100, Appl Sequence 320, Appl Sequence 100, Appl	ector-Mediated Delivery of Proapoptotic Genes	
9 US-09-779-050A-17 14 US-10-286-696-12 9 US-09-855-544A-10 16 US-09-855-544A-10 16 US-10-367-094-20 15 US-10-399-018-20 18 US-10-65-244-4 19 US-09-855-544A-9 19 US-09-855-544A-9 19 US-09-855-544A-9 14 US-10-389-224 14 US-10-050-902-224 14 US-10-050-902-224 14 US-10-050-908-224 15 US-10-050-908-224 16 US-10-050-908-224 17 US-10-289-456-101 18 US-10-289-456-101 19 US-09-933-915A-5 11 US-09-933-915A-5 11 US-09-933-915A-5 11 US-09-933-915A-5 11 US-09-933-915A-5 11 US-09-933-915A-6 12 US-10-289-456-103 13 US-09-933-915A-6 14 US-10-289-456-103 15 US-10-289-456-103 16 US-10-289-456-103 17 US-09-933-915A-4 18 US-10-289-456-103 19 US-09-933-915A-4 19 US-10-289-456-102 10 US-09-933-915A-4 11 US-09-933-915A-4 11 US-09-933-915A-4 11 US-09-933-915A-4 12 US-10-289-456-102	ALIGNMENTS 559 Treating Cancer B e Anti-Angiogenic 10/855,559 8 /475,006 ersion 4.0	7%; Pred. No. 2.3e-74; 5; Mismatches 13;
14 636 49.4 172 15 446 34.7 185 16 291 22.6 98 18 291 22.6 98 20 221 22.6 98 21 22.6 101 22 245.5 19.1 87 24 23.3 5 18.1 199 25 23.3 5 18.1 199 26 23.3 5 18.1 151 27 23.2 5 18.1 151 28 23.2 5 18.1 151 29 23.2 5 18.1 151 31 23.2 5 18.1 158 32 23.5 18.1 160 34 23.2 5 18.1 160 35 23.2 5 18.1 160 36 23.2 5 18.1 160 37 23.2 5 18.1 160 38 23.2 5 18.1 160 39 23.2 5 18.1 160 39 23.2 5 18.1 160 39 23.2 5 18.1 160 39 23.2 5 18.1 160 39 23.2 5 18.1 160 39 23.2 5 18.1 160 39 23.2 5 18.1 160 39 23.2 5 18.1 160 39 23.2 5 18.1 160 39 23.2 5 18.1 181 39 23.2 5 18.1 181 43 23.2 5 18.1 181 44 23.2 5 18.1 181	RESULT 1 US-10-855-559-4 US-10-855-559-4 Sequence 4, Application US/1085559 GENERAL INFORMATION: APPLICANT: Lalani, Alshad FILE OF INVENTION: Method for Tre TITLE OF INVENTION NUMBER: US/10/ CURRENT FILING DATE: 2003-06-03 NUMBER OF SEQ ID NOS: 30 SOFTWARE: FastSEQ for Windows Vers SEQ ID NO 4 TYPE: PRT TYPE: PRT GRGANISM: Homo sapien US-10-855-559-4 Query Match	Best Local Similarity 85. Matches 174; Conservative

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76 VRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGE 135
                                                                                                                                                     136 LVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLAKSARNSCWSK 195
                                                                                                                                                                               61 LVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDFILLMKSARNSCWSK 120
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                                                                           1 VRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGE
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  0; Indels
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Fatent No. US20020160416A1
GENERAL INFORMATION:
APPLICANT: BOYLE, WILLIAM
APPLICANT: BOYLE, MILLIAM
TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
FILE REFERENCE: A-570B
CURRENT APPLICATION NUMBER: US/09/779,050A
CURRENT FILING DATE: 2001-02-12
PRIOR APPLICATION NUMBER: 60/181,800
PRIOR FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PATENTIN VERSION 3.0
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  0; Mismatches
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APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin
APPLICANT: Marsters, Scot A.
APPLICANT: Pitti, Robert M.
APPLICANT: Wood, William
  Matches 168; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
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Publication No. US2005011328A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE Devi, Gayathri
TITLE OF INVENTION: Method and Antisense Compound for Potentiating Anti-Cancer Agents
TITLE SPERENCE: 50450.8058.0050
CURRENT APPLICATION NUMBER: US/10/981,989

CURRENT FILING DATE: 2004-11-04
PRIOR APPLICATION WINBER: 60/518,139
PRIOR APPLICATION NUMBER: 60/518,139
PRIOR APPLICATION OF: 14
                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Seol, Dae-Wu
APPLICANT: Seol, Dae-Wu
APPLICANT: Seol, Dae-Wu
APPLICANT: Seol, Dae-Wu
APPLICANT: Billiar, Timothy R.
TITLE OF INVENTION: DAR Cassette for the Production of
TITLE OF INVENTION: Secretable Recombinant Trimeric Trail Proteins, Tetracycline
TITLE OF INVENTION: Combination and Use in Gene Therapy
FILE REFERENCE: 5006-1-002
CURRENT APPLICATION NUMBER: US 2009-38441
PRIOR FILING DATE: 2002-03-19
PRIOR PLING DATE: 2000-07-06
NUMBER OF SEO ID NOS: 48
SOFTWARE: FastSEQ for Windows Version 4.0
                          146 NIKNDKOMVQXIXKYTSYPDPILLMKSARNSCWSKDAEYGLYSIYOGGIPELKENDRIFV 205
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161 NTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFV 220
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                                                                                                   221 SVTNEHLIDMDHEASFFGAFLVG 243
                                                                                                                                SVTNEHLIDMDHEASFFGAFLVG 228
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Patent No. US20020128438A1
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Best Local Similarity 100.
Matches 168; Conservative
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Matches 161; Conservative
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CORGANISM: Homo sapiens
US-10-338-083-11
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ORGANISM: Homo sapiens
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Best Local Similarity
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APPLICANT: Adhkenazi, Avi J.
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Scot A.
APPLICANT: Marsters, Scot A.
APPLICANT: Work I. Robert M.
APPLICANT: Work I. WOWEL THE SAME
ITILE OF INVENTION: ACIDS ENCODING THE SAME
CURRENT APPLICATION NUMBER: US/10/959,537
CURRENT PILING DATE: 2004-10-06
PRIOR FILING DATE: 1999-02-09
PRIOR PLING DATE: 1999-02-09
NUMBER OF SEQ ID NOS: 31
SEQ ID NO 29
LENGTH: 164
                                                                                                                                                                                                                                                                                80 GPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIH 139
                                                                                                                                                                                                                                                                                                                                                                        140 EKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEY 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 29, Application US/10959537
Publication No. US20050069983A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 99.4°
Matches 163, Conservative
                                                                                                     ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-116-378-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , ORGANISM: Homo sapiens
US-10-959-537-29
                                                                              LENGTH: 164
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GENERAL INFORMATION:
APPLICANT: Shu, Hong-Bing
ITILE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND
ITILE OF INVENTION: METHODS OF USE THEREOF
ITILE OF INVENTION: METHODS OF USE THEREOF
ICURENT APPLICATION NUMBER: US/10/216,074
CURRENT APPLICATION NUMBER: US/09/565,423
PRIOR APPLICATION NUMBER: US/09/565,423
PRIOR APPLICATION NUMBER: UNKNOWN
PRIOR FILING DATE: 2000-05-05
PRIOR FILING DATE: 2000-05-01
PRIOR FILING DATE: 2000-05-06
NUMBER OF FILING DATE: 1000-05-06
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PATENTIN VEY: 2.1
SOFTWARE: PATENTIN VEY: 2.1
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Sequence 11, Application US/10338083

Publication No. US20030166559A1

SERNERAL INFORMATION:
APPLICANT: Desjarlais, John R.
APPLICANT: Desjarlais, John R.
TITLE OF INVENTION: Deminant Negative Proteins and Methods Thereof
TITLE OF INVENTION: Deminant Negative Proteins and Methods Thereof
TITLE OF INVENTION: Deminant Negative Proteins and Methods Thereof
TITLE OF INVENTION: Deminant Negative Proteins and Methods Thereof
TITLE OF INVENTION: Deminant Negative Proteins and Methods Thereof
TITLE OF INVENTION NUMBER: US/10/338,083

PRIOR PELICATION NUMBER: US 60/345,805

PRIOR FILING DATE: 2002-01-04

PRIOR FILING DATE: 2002-01-04

PRIOR FILING DATE: 2002-01-04

NUMBER OF SEQ ID NOS: 23

SOFTWARE: Patentin Version 3.2

SEQ ID NO 11
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; SEQ ID NO 11
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-794-751-11
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Fublication No. US20040170602A1
GENERAL INFORMATION:
APPLICANT: Desjarials, John R.
APPLICANT: Desjarials, John R.
TITLE OF INVENTION: DOMINANT NEGATIVE PROTEINS AND METHODS THEREOF
ITTLE OF INVENTION: DOMINANT NEGATIVE PROTEINS AND METHODS THEREOF
CURRENT APPLICATION UNMBER: US/10/611,399
CURRENT FILING DATE: 2003-01-06
FRIOR APPLICATION NUMBER: US 60/345,805
FRIOR APPLICATION NUMBER: US 60/373,453
FRIOR APPLICATION NUMBER: US 60/373,453
FRIOR FILING DATE: 2002-04-17
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PATENTIN VERSION 3.2
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Sequence 11, Application US/10794751

Publication No. US20050048626A1

GENERAL INFORMATION:

APPLICANT: Desjarlais, John R.

APPLICANT: Thomason, Adam Read

APPLICANT: Thurmason, Adam Read

APPLICANT: Thurmason, Adam Read

TITLE OF INVENTION BAFF VARIANTS AND METHODS THEREOF

FILE REFERENCE: A-72175-1

CURRENT APPLICATION NUMBER: US/10/794,751

CURRENT APPLICATION NUMBER: US 60/452,707

PRIOR FILING DATE: 2003-01-06

PRIOR FILING DATE: 2003-03-07

PRIOR FILING DATE: 2003-03-07

PRIOR FILING DATE: 2003-05-23

PRIOR FILING DATE: 2003-05-23

PRIOR FILING DATE: 2003-11-20

PRIOR FILING DATE: 2003-12-08

NUMBER OF SEQ ID NOS: 23

SOFTWARE: PatentIn version 3.3
                                                            121 YSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV 161
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66.0%; Score 849; DB
Best Local Similarity 100.0%; Pred. No. 1.6
Matches 161; Conservative 0; Mismatches
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ORGANISM: Homo sapiens
                                                                                                                                                                                                    US-10-611-399-11
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J. GARBERAL I TSCHOPP, JURG

TITLE OF INVENTION: APRIL-A NOVEL PROTEIN WITH GROWTH EFFECTS

FILE REFERENCE: A049 US

CURRENT APPLICATION NUMBER: US/10/778,890

CURRENT FILING DATE: 2004-02-12

PRIOR PLILING DATE: 2004-02-12

PRIOR PLILING DATE: 2000-03-08

PRIOR PLILING DATE: 1998-09-11

PRIOR PLILING DATE: 1998-03-16

PRIOR PLILING DATE: 1998-03-26

PRIOR FILING DATE: 1998-03-2
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           Length 161;
                                                                                                                           Indels
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Query Match
Best Local Similarity 100.0%; Pred. No. 1.6e-70;
Matches 161; Conservative 0; Mismatches 0;
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TITLE OF INVENTION: SEQUENCES OF TRAIL VARIANTS
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Sequence 16, Application US/09855544A

Patent No. US20020061525A1

GENERAL INFORMATION:
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; Sequence 10, Application US/10778890
; Publication No. US20050112596A1
; GENERAL INFORMATION:
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Sequence 17, Application US/09779050A Patent No. US20020160416A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             126 PILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           105 -----ENTKONOKINKYTSYPD 125
                                                                                                                                                                                                                                                                                                                                                 39 TNELKQMQDKYSKSGIACPLKEDDSYMDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEE 98
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                                                                                                                                                                                                                                                                                                                         1 TNELKOMODKYSKSGIACFLKEDDSYWDPNDEESMNSPCWOVKWOLROLVRKMILRTSEE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TNELKOMODKYSKSGIACFLKEDDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEE
                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                   64.2%; Score 826; DB 9; Length 208; 96.3%; Pred. No. 3e-68; indels tive 4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 SCHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENT 162
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Fatent No. US20020061525A1
GENERAL INFORMATION:
APPLICANT:
FILE REFERENCE: 2786-0173P
CURRENT FILING DATE: 2001-05-19
CURRENT FILING DATE: 2001-05-19
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn Ver. 2.1
FILE REFERENCE: 2786-0173P
CURRENT PEDLICATION NUMBER: US/09/855,544A
CURRENT FILING DATE: 2001-05-19
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PATENTIN VET: 2.1
SEQ ID NO 16
LENGTH: 208
                                                                                                                                                                                                                                   Query Match
Best Local Similarity 96.33
Matches 156; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                   ORGANISM: Homo sapiens
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US-09-779-050A-17
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                                                                                                                                                   TYPE: PRT
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APPLICANT: Hou, Hailing
APPLICANT: How, Hailing
APPLICANT: How, Hailing
APPLICANT: Boyle, William J
TITLE OF INVENTION: Fhm. A No. US20030129706Alel Member of the TNF Ligand Supergene FF
FILE REFERENCE: 01017/35550A
CURRENT APPLICATION NUMBER: US/10/286,696
CURRENT FILING DATE: 2002-11-01
PRIOR FILING DATE: 1999-08-04
NUMBER OF SEQ ID NOS: 22
SOPTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81 PORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHE 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        141 KGFYYIYSQTYFRFQEE-----IKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWS 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49.4%; Score 636; DB 9; Length 172; 71.4%; Pred. No. 9.3e-51; tive 20; Mismatches 22; Indel8
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APPLICANT: BOYLE, WILLIAM
APPLICANT: BOYLE, WILLIAM
TITLE OF INVENTION: RECEPTOR FROM TWF FAMILY
FILE REFREENCE: A-5708
CURRENT APPLICATION NUMBER: US/09/779,050A
CURRENT APPLICATION NUMBER: 00/181,800
PRIOR APPLICATION NUMBER: 60/181,800
PRIOR FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PATENTIN VERSION 3.0
SOFTWARE: PATENTIN VERSION 3.0
LENGTH: 172
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US-10-286-696-12
US-10-286-696-12, Application US/10286696
; Publication No. US20030129706A1
; GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 71.43
Matches 120; Conservative
                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
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Appl Appl Appli Appli

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67 EKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFL 126
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APPLICANT: WILEY, S.R.
TITLE OF INVENTION: PENBER OF THE TNF FAMILY USEFUL
TITLE OF INVENTION: FOR TREATMENT AND DIAGNOSIS OF DISEASE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSES: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72.3%; Score 930; DB 3; Length 177; 99.4%; Pred. No. 1.6e-88; Live 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: TESTER Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,343A
FILING DATE: 12-FEB-1998
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US98/02859
FILING DATE: 12-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: BECKER, Cheryl L.
REGISTRATION NUMBER: 35,441
REGISTRATION NUMBER: 35,441
REGISTRATION NUMBER: 6048.US.P2
TELECOMMUNICATION INFORMATION:
             US-08-630-172-5

US-09-375-419-5

US-09-375-419-5

US-09-384-65-17

US-09-934-465-17

US-09-939-214-4

US-08-339-214-4

US-08-339-214-8

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: No. 6207642e
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STRANDEDNESS:
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STATE: IL
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Sequence 12, Appl
Sequence 12, Appl
Sequence 31, Appl
Sequence 4, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 1, Appli
Sequence 11, Appli
Sequence 10, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 16, Appli
Sequence 18, Appli
Sequence 18, Appli
Sequence 18, Appli
Sequence 20, Appli
Sequence 20, Appli
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Sequence 7, Appli
                                                                                                        3, 2005, 06:38:16 ; Search time 42 Seconds (without alignments)
431.898 Million cell updates/sec
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1287
1 TNBLKQMQDKYSKSGIACFL......NBHLIDMDHBASFFGAFLVG 243
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Sequence
Sequence
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1: /cgn2_6/ptodata/1/laa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/laa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/laa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
                GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-565-423-7
US-09-105-343A-8
US-09-105-343A-8
US-09-569-611C-29
US-09-569-611C-32
US-09-569-611C-32
US-09-569-611C-32
US-09-369-611C-32
US-09-36-611C-31
US-09-36-611C-31
US-09-36-937-10
US-09-36-937-14
US-09-396-937-14
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US-09-254-180C-176
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Listing first 45 summaries
                                                                               protein search, using sw model
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Maximum Match 100
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Match Length DB
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Maximum DB seq length: 243
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CURRENT APPLICATION DATA:
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181 II 182
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                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Shu, Hong-Bing
TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND
TITLE OF INVENTION: METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 120
                                                                                 61 SNIJHLRUGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQNVQYIYKYTSYPDFILLMK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           143 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 202
1 EKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                           187 SARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 243
                                                                                                                                                                1 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
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DIAGNOSIS OF DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        203 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.0%; Pred. No. 2.9
Matches 161; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 8, Application US/09105343A
Patent No. 6207642
GENERAL INFORMATION:
APPLICANT: WILEY S.R.
TITLE OF INVENTION: FOR TREATMENT AND DIA
TITLE OF INVENTION: FOR TREATMENT AND DIA
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSER: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park Road
STREET: ILL
                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 2879-72
CURRENT APPLICATION NUMBER: US/09/565,423
CURRENT FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: UNKNOWN
PRIOR FILING DATE: 2000-05-01
PRIOR FILING DATE: 1999-05-06
                                                                                                                                                                                                                                                              US-09-565-423-7
; Sequence 7, Application US/09565423
; Patent No. 6475987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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US-09-105-343A-8
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127 SNLHLRNGELVIHEKGFYYIYSQTYFRFQEE-----IKENTKNDKQMVQYIYKYTSYPD 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67 EKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFL 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 TISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSK 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 50.8%; Score 654; DB 3; Best Local Similarity 68.7%; Pred. No. 7.6e-60; Matches 125; Conservative 22; Mismatches 29
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                FILING DATE: 12-FEB-1998
CLASSIFICATION DATE: 1998
PRIOR APPLICATION DATE: APPLICATION NUMBER: PCT/US98/02859
ATTORNEY, AGENT INFORMATION: NAME: BECKER, Cheryl L. REGISTRATION NUMBER: 35,441
REFRERENCE/DOCKER NUMBER: 35,441
TELECOMUNICATION INFORMATION: TELECOMUNICATION INFORMATION: TELECOMUNICATION INFORMATION:
US/09/105,343A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: No. 6207642e
                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 183 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
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TELEX:
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39 TNELKQMQDKYSKSGIACFLKEDDSYMDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEE 98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TNELKOMODKYSKSGIACFLKEDDSYWDPNDEESMNSPCWQVKWQLRQLVRKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-670-354-4
; Sequence 4, Application US/08670354
; Patent No. 576323.3
; GENERAL INFORMATION:
APPLICANT: Steven R. Wiley and APPLICANT: Raymond G. Goodwin.
TITLE OF INFORTION: Cytokine That Induces Apoptosis
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
STREET: 51 University Street
                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: SAVITZATY et al.
TITLE OF INVENTYON: ALTERNATIVE SPLICING VARIANTS
FILE REFERENCE: 2786-0151P
CURRENT APPLICATION NUMBER: US/09/569,611C
CURRENT FILING DATE: 2000-05-10
NUMBER OF SEQ ID NOS: 52
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 292; DB 4;
Pred. No. 1.5e-22;
1; Mismatches 0
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MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/670,354
FILING DATE: 25-JUN-1996
CLASSIFICATION APTA:
APPLICATION NUMBER: US 08/496,632
FILING DATE: 29-JUN-1995
CLASSIFICATION: 435
CLASSIFICATION NUMBER: US 08/496,632
FILING DATE: 29-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/548,368
FILING DATE: 01-NOV-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                  Sequence 32, Application US/09569611C Patent No. 6720182
                                                                                                                                               99 TISTVQEKQQNISPLVRERG 118
                                                                                                              61 TISTVĢEKQQNISPLVRERG 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22.7%;
98.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-569-611C-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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US-09-569-611C-32
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STATE: WA
COUNTRY:
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Matches
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APPLICANT: Hou, Hailing
APPLICANT: Wooden, Scott K
APPLICANT: Boyle, William J
TITLE OF INVENTION: Fhm, A No. 6521422el Member of the TNF Ligand Supergene Family
FILE REFERENCE: 01017/35550A
CURRENT APPLICATION NUMBER: US/09/632,287A
CURRENT FILING DATE: 2000-08-03
PRIOR PRIOR DATE: 1999-08-04
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7833, Application US/09513999C

Patent No. 6783961

GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Ducert, A.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FILE REPERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT PILING DATE: 2000-02-24
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 7833
LENGTH: 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78 ERGPORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELV 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELV 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34.7%; Score 446; DB 4; Length 85; 100.0%; Pred. No. 9.6e-39; Live 0; Mismatches 0; Indels
123 TISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSR 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: -32..-1
OTHER INFORMATION: SCORE 5.3
OTHER INFORMATION: SEQ VIFTVLLQSLCVA/VT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 IHEKGFYYIYSQTYPRFQEEIKENT 85
                                                                                                            Sequence 12, Application US/09632287A
Patent No. 6521422
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US-09-513-999C-7833
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Best Local Similarity 100..
Thes 85; Conservative
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 80; Conserv
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NAME/KEY: SIGNAL
LOCATION: -32..-1
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TYPE: PRT
ORGANISM: human
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                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                        1 TNELKOMODKYSKSGIACFLKEDDSYWDPNDEBSMNSPCWQVKWQLRQLVRK 52
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                                                                                                                                                                                                                                                                                                        Length 101;
                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/09320424

| Sequence 4, Application US/09320424
| Patent No. 6284236
| GENERAL INFORMATION:
| APPLICANT: Wiley, Steven R.
| APPLICANT: Wiley, Steven R.
| TITLE OF INVENTION: Cytokine that Induces Apoptosis FILE REPERENCE: 2835-E
| CURRENT APPLICATION NUMBER: US/09/320,424
| CURRENT FILING DATE: 1999-05-26
| EARLIER APPLICATION NUMBER: 09/190,046
| EARLIER PELING DATE: 1998-11-10
| EARLIER FILING DATE: 1998-03-26
| EARLIER FILING DATE: 1998-11-01
| EARLIER FILING DATE: 1995-11-01
| EARLIER FILING DATE: 1995-11-01
| EARLIER FILING DATE: 1995-06-29
| NUMBER OF SEQ ID NOS: 25
| SEQ ID NO 4
| LENGTH: 101
| TVOE: DATE: 100
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; Batent No. 6521228
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; APPLICANT: Goodwin, Raymond G.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis; FILE REPERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/09/825,563
; CURRENT FILING DATE: 2001-04-02
; PRIOR PILING DATE: 1999-05-26
                                                                                                                                                                                                                                                                                                        Query Match 22.6%; Score 291; DB 1; I
Best Local Similarity 100.0%; Pred. No. 1.5e-22;
Matches 52; Conservative 0; Mismatches 0;
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ive 0; Mismatches
REFERENCE/DOCKET NUMBER: 2835-B
                               TELEFAX: (2000)
TELEFAX: 756822
; INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS: LENGTH: 101 amino acids "VPE: amino acid                    TELECOMMUNICATION INFORMATION TELEPHONE: (206) 587-0430 TELEFAX: (206) 233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 22.6
Best Local Similarity 100.
Matches 52; Conservative
                                                                                                                                                                                                      ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-670-354-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: human
US-09-320-424-4
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1 TNELKQMQDKYSKSGIACFLKEDDSYWDPNDEESMNSPCWQVKWQLRQLVRK 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
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Sequence 4, Application PC/TUS9610895
GENERAL INFORMATION:
APPLICANT: Immunex Corporation.
TITLE OF INVENTION: Cytokine That Induces Apoptosis NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSES: Kathryn A. Anderson, Immunex Corporation STREET: 51 University Street
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22.6%; Score 291; DB 4; ]
100.0%; Pred. No. 1.5e-22;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: WA

ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATIG SYSTEM: Apple 7.5.2
SOFTWARE: Microsoft Word, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10895
FILING DATE: 25-JUN-1996
CLASSIFICATION NUMBER: US 08/496,632
FILING DATE: 29-JUN-1995
CLASSIFICATION NUMBER: US 08/496,632
FILING DATE: 29-JUN-1995
CLASSIFICATION NUMBER: US 08/548,368
FILING DATE: 01-NOV-1995
CLASSIFICATION NUMBER: US 08/548,368
FILING DATE: 01-NOV-1995
CLASSIFICATION:
PRIOR APPLICATION NUMBER: 09/190,046
PRIOR FILING DATE: 1998-11-10
PRIOR PELLIANG DATE: 1998-11-10
PRIOR PELLIANG DATE: 1998-03-26
PRIOR FILING DATE: 1996-06-25
PRIOR APPLICATION NUMBER: 08/570,354
PRIOR APPLICATION NUMBER: 08/548,368
PRIOR PILING DATE: 1995-11-01
PRIOR FILING DATE: 1995-11-01
PRIOR FILING DATE: 1995-06-29
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PALENTIN VET: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2835-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 101 amino acids
amino acid
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Matches 52, Conservative
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INFORMATION FOR SEQ ID NO:
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GENERAL INFORMATION:
APPLICANT: MAE Biotech A/S
APPLICANT: MAE Biotech A/S
APPLICANT: HALKIER, Torben
APPLICANT: HAANING, Jesper
TITLE OF INVENTION: Method for Down-Regulating Osteoprotegerin Ligand
TITLE OF INVENTION: Activity
FILE REFERENCE: 22021 PC 1
                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Description of Artificial Sequence: DNA encoding ; OTHER INFORMATION: murine OPGL, residues 158-316, fused to His tag US-09-396-937-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 17.8%; Score 228.5; DB 4; Length 173; Best Local Similarity 34.2%; Pred. No. 1e-15; Matches 54; Conservative 31; Mismatches 62; Indels 11;
                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/396,937
CURRENT FILING DATE: 1999-09-15
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 10
LENGTH: 173
              Sequence 10, Application US/09396937
Patent No. 6645500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 12, Application US/09396937 Patent No. 6645500
                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
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US-09-396-937-12
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                                                                                                                                                                                                                                                                                                                                      LENGTH:
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Sequence 13. Application US/09632287A

Sequence 13. Application US/09632287A

Sequence 13. Application US/09632287A

Sequence 13. Application US/09632287A

GENERAL INFORMATION:

APPLICANT: Hou, Hailing

APPLICANT: Boyle, William J

TITLE OF INVENTION: Fhm, A No. 6521422el Member of the TNF Ligand Supergene Family

FILE REFERENCE: 01017/35550A

CURRENT PILING DATE: 2000-08-03

PRIOR APPLICATION NUMBER: US 60/147,294

PRIOR FILING DATE: 1999-08-04
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                                                                Gaps
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                                                                                                           1 TNELKOMODKYSKSGIACFLKEDDSYWDPNDEESMNSPCWQVKWQLRQLVRK 52
                                                                                                                                          39 TNELKQMQDKYSKSGIACFLKEDDSYWDPNDEESMNSPCWQVKWQLRQLVRK 90
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                Score 291; DB 5; Length 101;
Pred. No. 1.5e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 22.6%; Score 291; DB 4; Length 122; Best Local Similarity 100.0%; Pred. No. 2e-22; Matches 52; Conservative 0; Mismatches 0; Indels
                                                           0; Indels
                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: SAVITZKY et al.
TITLE OF INFORMATION: ALTERNATIVE SPLICING VARIANTS
FILE REFERENCE: 2786-0151P
CURRENT APPLICATION NUMBER: US/09/569,611C
CURRENT FILING DATE: 2000-05-10
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PATENTIN VET. 2.0
22.6%; Scor.
100.0%; Pred. No. ...
'... 0; Mismatches
                                                                                                                                                                                                                                                                 Sequence 31, Application US/09569611C Patent No. 6720182
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         Query Match
Best Local Similarity 100."
Matches 52, Conservative
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Best Local Similarity 65.8°
Matches 50; Conservative
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LENGTH: 122
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LENGTH: 87
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146 IYSQTYFRFQEEIKENTKNDKQMVQYIYKYT-SYPDPILLMKSARNSCWSKDAEYGLYSI 204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22 AHLT-----INAASIPSGSHKVTL----SSWYHDR-GWAKISNWTLSNGKLRVNQDGFYY 71
                                        86 AHITGTRGRSWTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFYY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: MAE Biotech A/S
APPLICANT: HALKIER, Torben
APPLICANT: HALKIER, Torben
APPLICANT: HALKIER, Torben
APPLICANT: HALKIER, Torben
TITLE OF INVENTION: Method for Down-Regulating Osteoprotegerin Ligand
TITLE OF INVENTION: Activity
FILE REFERENCE: 22021 PC 1
CURRENT APPLICATION NUMBER: US/09/396,937
CURRENT FILING DATE: 1999-09-15
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PATENTIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Description of Artificial Sequence: Fusion of OTHER INFORMATION: murine OPGL, residues 158-316 with C to S OTHER INFORMATION: mutation, and His tag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 17.8%; Score 228.5; DB 4; Length 173; Best Local Similarity 34.2%; Pred. No. 1e-15; Matches 54; Conservative 31; Mismatches 62; Indels 11.
                                                                                                                                                                                                                                                              205 YQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV 242
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RESULT 14

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146 IYSQTYFRFQEEIKENTKNDKQMVQYIYKYT-SYPDPILLMKSARNSCWSKDAEYGLYSI 204 :|: || || :: |: || || || ||
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Search completed: June 3, 2005, 06:53:39 Job time: 43 secs

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US-09-513-999C-7833

US-09-56-611C-32

US-08-670-354-4

US-09-320-424-4

US-09-825-563-4

PCT-US96-11095-4

US-09-569-611C-31

US-09-569-611C-31

US-09-632-287A-12

US-09-632-287A-12

US-09-659-11

US-09-659-11

US-09-577-780-11

US-09-577-780-11

US-09-577-780-11

US-09-877-650-11

US-09-871-856-11

US-09-871-856-11

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US-09-871-650-11

US-09-871-650-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 281 amino acids
TYPE: amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein US-08-670-354-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
TOPOLOGY: linear
     258 8.5
258 8.5
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     118, App
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487.823 Million cell updates/sec
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Sequence 4, Al
Sequence 2, Al
Sequence 30, Al
Sequence 11, Al
Sequence 11, Al
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Sequence 2, 1
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. /cgn2 6/ptodata1/iaa/5A COMB.pep:*
: /cgn2 6/ptodata1/iaa/5B COMB.pep:*
. /cgn2 6/ptodata1/iaa/6A_COMB.pep:*
: /cgn2 6/ptodata1/iaa/6B_COMB.pep:*
: /cgn2 6/ptodata1/iaa/RB_COMB.pep:*
: /cgn2 6/ptodata1/iaa/PCTUS COMB.pep:*
                GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-934-465-1
US-10-011-125A-4
PCT-US96-10895-2
US-09-072-993C-3
US-09-569-611C-30
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US-09-825-563-2
US-09-919-039-118
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US-09-825-563-11
US-09-320-424-13
US-09-825-563-13
US-09-105-343A-7
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US-09-105-343A-8
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US-09-333-593A-6
                                                                                                                                                                                                                             513545 segs, 74649064 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                  OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
                                                                                                                                         US-10-662-431-2
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Match
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1000.0
1000.0
99.4
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1238
988
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100.0%; Score 1478; DB 1; Length 281;
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple machincoh
OPERATING SYSTEM: Apple machincoh
OPERATING SYSTEM: Apple machincoh
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/670,354
FILING DATE: 25-JUN-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/496,632
FILING DATE: 29-JUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/548,368
FILING DATE: 29-JUN-1995
CLASSIFICATION NUMBER: US 08/548,368
FILING DATE: 01-NOV-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REBRENCE/DOCKET NUMBER: 32,172
RELEPHONE: (206) 587-0430
TELLERAX: (206) 233-0644
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61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
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Sequence 10, Application US/08883086

Patent No. 617187

GENERAL INFORMATION:

APPLICANT: WILEY, STEVEN

TITLE OF INVENTION: FOR TREATMENT AND DIAGNOSIS OF DISEASE

NUMBER OF SEQUENCES: 13

CORRESCONDENCE ADDRESS:

ADDRESSEE: Abbott Laboratories

STREET: 100 Abbott Park Road

CITY: Abbott Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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100.0%; Score 1478; DB 3;
Best Local Similarity 100.0%; Pred. No. 3.5e-149;
Matches 281; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                          MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: 18M PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: MinPatin (Genentech) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/780,496 FILING DATE: 08-Jan-1997 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: Marschang, Diane L. REGISTRATION NUMBER: 35,600 REGISTRATION NUMBER: 35,600 REPRENNE/DOCKTAIN NUMBER: 910/371-7168 TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION FOR SEQ. 19 10/371-7168 INFORMATION FOR SEQ. 10 NO: 1: SEQUENCE CHARACTERISTICS:
                  NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSE: Genertech, Inc.
STREET: Gent San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb flog
Apo-2 Ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 281 amino acids
Amino Acid
  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: Linear
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Patent No. 6046048
GENERAL INFORMATION:
APPLICANT: Avi Ashkenazi, Anan Chuntharapai, Kyung Jin Kim
                            Indels
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                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08584031A
Patent No. 6030945
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: APD-2 LIGAND
FILE REFERRNCE: 11669.22US03
CURRENT APPLICATION NUMBER: US/08/584,031A
CURRENT FILING DATE: 1996-01-09
CURRENT FILING DATE: 1996-01-09
SOFTWARE: Patentin Ver. 2.0
  100.0%;
                         Matches 281; Conservative
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ORGANISM: Homo sapiens
  Best Local Similarity
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Gaps

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241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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EARLIER FILING DATE: 1995-11-01
BARLIER APPLICATION UNBER: 08496,632
EARLIER FILING DATE: 1995-06-29
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 281
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Best Local Similarity 100.
Matches 281; Conservative
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ORGANISM: HOMO SAPIENS
                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: human
US-09-320-424-2
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APPLICANT: Goodwin, Raymond G.
TITLE OF INVENTION: CYTCKINE that Induces Apoptosis
FILE REFERENCE: 2835-E
CURRENT APPLICATION NUMBER: US/09/320,424
CURRENT FILING DATE: 1999-05-26
EARLIER FILING DATE: 1998-11-10
EARLIER FILING DATE: 1998-11-10
EARLIER FILING DATE: 1998-03-26
EARLIER FILING DATE: 1998-03-26
EARLIER FILING DATE: 1996-06-25
EARLIER APPLICATION NUMBER: 08/670,354
EARLIER APPLICATION NUMBER: 08/670,354
EARLIER APPLICATION NUMBER: 08/670,354
                                                                                                                                                                                                                                                                                             FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: POFEMBER; Friscilla E.
REGISTRATION NUMBER: 33,207
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-937-0378
TELEFAX: 847-938-2623
                                                                COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastEGQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/883,086
FILING DATE:
CLASSIFICATION: 424
PROR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/09320424
Patent No. 6284236
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear _ MOLECULE TYPE: No. 6171787e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: amino acid
                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: single
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                                                                                                                                                  1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKB
                                                                                                                                                                                                                                                                                                                                              121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
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                                                                                                               1 MAMMEVOGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
                                                                Gaps
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APPLICANT: YOUNG, PETER R.

APPLICANT: YOUNG, PETER R.

APPLICANT: ROSHAK, AMY K.

APPLICANT: TAN, KONG B.

APPLICANT: TRUNEH, ALEMBGED

TITLE OF INVENTION: TWOR B-CTOR RELATED RECEPTOR,

TITLE OF INVENTION: TROMBER: US/09/333,593A

CURRENT APPLICANTON NUMBER: US/09/333,593A

CURRENT FILING DATE: 1999-06-15

PRIOR APPLICATION NUMBER: 08/16,625

PRIOR PELING DATE: 1997-08-22

PRIOR FILING DATE: 1997-08-12

PRIOR FILING DATE: 1997-03-14

SOFTWARE: FASTERQ FOR WINGOME VERSION 3.0

SEQ ID NO 6

SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 1478; DB 3; Length 281; 100.0%; Pred. No. 3.5e-149; ive 0; Mismatches 0; Indels 0;
100.0%; Score 1478; DB 3; Length 281; 100.0%; Pred. No. 3.5e-149; ive 0; Mismatches 0; Indels 0.
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RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
                       61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
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                                                                                        FYXIYSQTYFRFQEEIKENTKNDKQMVQXIYKYTSYPDPILLMKSARNSCWSKDAEYGLY
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Pred. No. 3.5e-149;
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                                                                                                                                                                                   241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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APPLICANT: WILLS.
APPLICANT: WILLS.
TITLE OF INVENTION: Cytokine that Induces Apoptosis
FILE REFERENCE: 2835-E
CURRENT APPLICATION NUMBER, US/09/825,563
CURRENT FILING DATE: 1099-05-26
PRIOR RELIGN DATE: 1999-05-26
PRIOR RELIGN DATE: 1999-01-10
PRIOR RELING DATE: 1999-05-66-10
PRIOR RELING DATE: 1998-03-26
PRIOR RELING DATE: 1998-03-26
PRIOR RELING DATE: 1996-06-25
PRIOR RELING DATE: 1996-06-25
PRIOR FILING DATE: 1995-11-01
PRIOR APPLICATION NUMBER: 08/548,368
PRIOR FILING DATE: 1995-06-25
PRIOR FILING DATE: 1995-06-25
PRIOR APPLICATION NUMBER: 08/548,368
PRIOR FILING DATE: 1995-06-29
PRIOR APPLICATION NUMBER: 08/546,632
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100.0%; Score 1478;
Best Local Similarity 100.0%; Pred. No. 3.5
Matches 281; Conservative 0; Mismatches
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US-09-919-039-118
; Sequence 118, Application US/09919039
                                                                                                                                                                                                                                                                                                                                            2, Application US/09825563
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                                                                                                                                                                                                                                                                                                                      -09-825-563-2
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                                                                                                                       DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
                                                                                        RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
                                                                                                                                                                                   FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
                                                                                                                                                                                                                              181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDFILLMKSARNSCWSKDAEYGLY 240
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ADDRESSEE: Legal Services
STREET: 301 Henrietta Street
                                                                                                                                                                                                                                                                              SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/157,864
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100.0%; Pred. No. 3.5e-149;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Bienkowski, Michael J
APPLICANT: Mills, Cynthia J
APPLICANT: Jones, David A
TITLE OF INVENTION: TNF-Related Death Ligand
WUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6111.N CN1
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IBM PC compatible
:YSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-157-864-11
; Sequence 11, Application US/09157864
Patent No. 6440694
; GENERAL INFORMATION:
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ATTORNEY/AGENT INFORMATION:
NAME: Kerber, Lori L.
REGISTRATION NUMBER: 41,113
REFERENCE/DOCKET NUMBER: 6111
TELECOMMUNICATION INFORMATION:
TELEPHONE: 616/833-0974
TELEPHONE: 616/833-8897
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INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 281 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0
Matches 281; Conservative
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER:
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TELEX: 23
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61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
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                              1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
                                                                                                                                                                                                                          121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
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  MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
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TITLE OF INVENTION: APO-2 LIGAND
FILE REPERENCE: 11669.22033
CURRENT APPLICATION NUMBER: US/09/934,465
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: 08/584,031
PRIOR APPLICATION NUMBER: 08/584,031
PRIOR APPLICATION NUMBER: 08/584,031
PRIOR PILING DATE: 1996-01-09
SEQ ID NO: SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: LENGTH: 281
TYPE: PRT

ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 11
US-09-934-465-1
Sequence 1, Application US/09934465
Patent No. 6746666
GENERAL INFORMATION:
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US-10-011-125A-4
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  APPLICANT: Kaser, Matthew R.
TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES FILE REFERENCE: PA-0035 US
CURRENT APPLICATION NUMBER: 08/09/919,039
CURRENT FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: 60/222,113
PRIOR APPLICATION NUMBER: 60/222,113
SOFTWARE: PERL PROGram
SEQ ID NOS: 401
SEQ ID NO: 401
SEQ ID NO: 401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 281;
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                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6727066 059509CD1
US-09-919-039-118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GREERAL INCORNATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Kelley, Robert F.
APPLICANT: O'Connell, Mark P.
APPLICANT: O'Connell, Mark P.
APPLICANT: Schwall, Ralph H.
ITLE OF INVENTION: APO-2 Ligand
FILE REFERENCE: P0978P4
CURRENT APPLICATION NUMBER: US/09/582,450
CURRENT FILING DATE: 2001-05-14
PRIOR APPLICATION NUMBER: US 09/007,886
PRIOR PRILING DATE: 1998-01-15
PRIOR APPLICATION NUMBER: US 09/060,533
PRIOR FILING DATE: 1998-04-15
PRIOR FILING DATE: 1998-04-15
SEQ ID NO 1
LENGTH: 281
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US-09-582-450-1
'Sequence 1, Application US/09582450
'Patent No. 6740739
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 281; Conservative
                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
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GENERAL INFORMATION:
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100.0%; Score 1478; DB 4; Length 281; 100.0%; Pred. No. 3.5e-149; tive 0; Mismatches 0; Indels 0
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TELECOMMUNICATION INFORMATION:
                                                     TELEX: 756822
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: amino acids
                      (206) 587-043
(206) 233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 279; Conservative
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TYPE: PRT
ORGANISM: HOMO SAPIENS
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                      TELEPHONE:
TELEFAX: (2
TELEX: 7568
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                                                                                                                                                                                                                                       Length 281;
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APPLICANT: Immunex Corporation.
TITLE OF INVENTION: Cytokine That Induces Apoptosis
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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                                                                                                                                                                                                                                     ; Score 1478; DB 4;
; Pred. No. 3.5e-149;
0; Mismatches 0;
; TITLE OF INVENTION: BACTERIAL HOST STRAINS; FILE REFERENCE: P1804R1
; CURRENT APPLICATION NUMBER: US/10/011,125A
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: US 60/256,162
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 12
; LENGTH: 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: Apple 7.5.2
SOFTWARE: Microsoft Word, Version 6.0.1
CURRENT APPLICATION DATA:
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APPLICATION UNDBER: US 08/496,632
FILING DATE: 29-JUN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/548,368
FILING DATE: 01-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/US96/10895
FILING DATE: 25-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2835-WO
                                                                                                                                                                                                                                       100.08;
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MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
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Best Local Similarity 100.0
Matches 281; Conservative
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CLASSIFICATION:
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CITY: Seattle
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Sequence 3, Application US/09072993C
Patent No. 634638
GENERAL INFORMATION:
APPLICANT: Michael R. Brigham-Burke
APPLICANT: Peter R. Young
TITLE OF INVENTION: A METHOD OF IDENTIFYING AGONIST AND
TITLE OF INVENTION: A METHOD OF TUMOR NECROSIS RELATED RECEPTORS TR1 AND TR2
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Query Match 100.0%; Score 1478; DB 5; Length 281; Best Local Similarity 100.0%; Pred. No. 3.5e-149; Matches 281; Conservative 0; Mismatches 0; Indels 0.
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CURRENT APPLICATION NUMBER: US/09/072,993C
CURRENT FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/055,513
PRIOR PELING DATE: 1997-08-13
PRIOR PELING DATE: 1997-08-26
PRIOR FILING DATE: 1997-08-26
PRIOR FILING DATE: 1997-08-26
PRIOR FILING DATE: 1997-08-29
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FASELSEQ for Windows Version 3.0
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SYMDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQRV 120
                                                                   121 AAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFY 180
                                                                                                                          61 DDSYMDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
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                                          AAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFY
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85.4%; Pred. No. 1.3e-123;
tive 2; Mismatches 5; Indéle 36
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US-09-569-611C-30

//S-09-569-611C-30

//Sequence 30, Application US/09569611C

//Sequence 30, Application US/09569611C

//Sequence 30, Application US/09569611C

//SEQUENCE INFORMATION:

//APLICANT: SAVITZKY et al.

//TITLE OF INVENTION: ALTERNATIVE SPLICING VARIANTS

//STILE REPERENCE: 2786-0151P

//CURRENT APPLICATION UNMBER: US/09/569,611C

//CURRENT FILING DATE: 2000-05-10

//SEQ ID NOS: 52

//SEQ ID NOS: 52

//SEQ ID NOS: 230

//SEQ ID NOS: 211
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Best Local Similarity 85.4
Matches 240; Conservative
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ORGANISM: Homo sapiens
US-09-569-611C-30
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Search completed: June 3, 2005, 06:26:29 Job time : 45 secs This Page Blank (uspto)